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October 4, 2002, 10:12:27; Search time 29.49 Seconds (without alignments) 741.999 Million cell updates/sec
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197
1 SQPQAVPPYASENQTCRDQE......QSDTTCKNPLEPLPPEMSGT 197
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                    OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Extracellular doma	Human lymphotoxin	TNF-R extracellula	Human TNF-R extrac	TNFR molecule LT-b	Human tumour necro	Human neurofilamen	Propionibacterium	Novel human diagno	Propionibacterium	Novel human diagno
SUMMARIES	AAW23220	AAY31326	AAW94642	AAB69194	AAU04498	AAB36700	AAY20502	AAU65981	ABG20744	AAU58231	ABG08131
DB	18	20	20	22	22	22	. 61	22	22	22	22
% Query Match Length DB ID	197	197	77	77	38	415	71	75	80	94	104
% Query Match	100.0	100.0	39.1	39.1	9.6	5.1	3.6	3.6	3.6	3.6	3.6
Score	197	197	77	77	19	10	7	7	7	7	7
Result No.		7	m	4	5	9	7	80	6	10	11

Propionibacterium Novel human diaqno	human	dopsis	Novel human diagno		Arabidopsis thalia	Arabidopsis thalla	ß	Arabidopsis thalia	Alpha-amylase-8-C.	Rice alpha-Amy8-C	Rice alpha-amylase	Alpha-amylase rela	C glutamicum prote	Maize 4-coumarate:	Human pif-1 type h	Drosophila melanog	Staphylococcus aur	Myxoma virus immun	Amino acid sequenc	Primer generating	Human complementar	Reactive peptide w	Sequence of synthe	Sequence of synthe	Sequence of synthe	oĘ		οţ	. Peptide used In pr	peptide		N-terminal peptide
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AAU50142 ABG01762	ABG05157	AAG55558	9 /	AAG15889	AAG5557	AAG55556	AAG15888	AAG15887	AAR76521	AAB12799	AAM50252	AAB97246	AAG91139	AAY05657	AAE01020	ABB62427	AAU37362	AAB61853	AAB07665	AAR79485	AAG97202	AAY93840	AAR28478	AAR28479	AAR28480	AAR28481	AAR28482	AAR28483	AAW41620	AAB66972	AAP81130	AAR25941
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ALIGNMENTS

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                                                                                                              The present sequence, a human lymphotoxin beta receptor (LT-beta-R) blocking agent, comprises the extracellular ligand binding domain of the human LT-beta-R up to the transmembrane region. It can be used to treat a Thl cell mediated immune response which contributes to a delayed type hypersensitivity reaction, preferably contact, thereulin type or granulomatous hypersensitivity, graft versus host disease, organ rejection or an autoimmune disorder, i.e. multiple sclerosis, insulin dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can also be used to treat conditions exacerbated by the activities of Th-1 type cytokines, or Listeria, Toxoplasma or Mycobacterium infection. Its ability to selectively or partially block the LT-beta-R pathway may be useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell; immune system; tumour; follicular lymphoma; extracellular domain; human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                       with missexpression or overexpression of signalling by the LT-beta-R pathway. The present LT-beta-R blocking agent is capable of selectively inhibiting Thi, but not Th2 cell dependent immune effector mechanisms. As Thi cytokines can inhibit Th2 cell dependent responses, the present LT-beta-R blocking agent may also indirectly stimulate certain Th2 cell dependent responses which are normally inhibited by Th1 induced cytokines. Doses of about 1 mg/kg of the present soluble LT-beta-R are expected to be suitable starting doses for optimising treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 sqpqavppyasenqtcrdqekeyyepqhriccsrcppgtyvsakcsrirdtvcatcaens 60
comprising lymphotoxin-beta receptor blocking agent auto:immune diseases, e.g. sclerosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 197;
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                                                                             Example 1; Pages 55-56; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY31326 standard; peptide; 197 AA.
                                    insulin-dependent diabetes, etc.
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  Compositions
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The invention provides a method for arresting or reducing, severity of the fletts of a tumnour by administration of a composition which inhibits the interaction between lymphotoxin (LT)-beta and its receptor. An inhibitor of the interaction between LT-beta and its receptor can be administered for altering the survival or maintenance of follicular dendritic cells in a subject and for altering the architecture of the organs of the immune system. The method is useful for traditing tumours, specifically follicular lymphomas. It offers an alternative therapy for hose with tumours resistant to traditional chemotherapy. The present sequence represents the extracellular region of the human LTbeta-receptor and comprises the ligand binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YNEHWNYLTICQLCRPCDPVMGLBEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 cppgteaelkdevgkgnnhcvpckaghfqntsspsarcqphtrcengglveaapgtagsd 180
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                                                                                                                                                                                        New method of treating follicular lymphomas by inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation; septic shock; cachexia; graft versus host skih allergic reaction; immune complex disease; malaria;
                                                                                                                                                                                                            interaction between lymphotoxin-beta and its receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 197; DB 20;
Pred. No. 4.2e-200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNF-R extracellular Cys-rich domain TNF-R-rp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                      Tsiagbe V;
                                                                                                                                                                                                                                                   Example 1; Page 25-26; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
98US-0073410
98US-0073112
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Best Local Similarity 100.
Matches 197; Conservative
                                                                                                                                               WPI; 1999-469242/39.
                                                            (BIOJ ) BIOGEN INC.
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02-FEB-1998;
30-JAN-1998;
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                                                                                                      Browning J,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A polypeptide comprising the isolated amino acid sequence of a pre-ligand assembly domain (PLAD) of a TNF-like receptor for inhibiting TNF receptor or Fas oligomerisation in a cell and for treatment of
                               anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
gene therapy; restenosis; graft versus host disease; tumour; cancer;
                                                                                                                       Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic; TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic;
                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                 15-MAR-2001
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      apoptotic
                                                                                                                                                                                                                                                                                                                                                                       AAB36700;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAB36700 standard;
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                                                                                              lmmunosuppressive; neuroprotective; antiviral; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
         therapy; ;
totic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPPGTYVSAKCSRIRDTVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cppgtyvsakcsrirdtvc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and thyroiditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US04125
                                                                                                                                                                                                                                               necrosis factor receptor LTbR protein SEQ ID NO:6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=
10
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                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myasthenia gravis,
            related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Siegel RM
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                                                                                                                                                                                                                                                                                                                                                                                                                                   415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19;
Pred. No.
         disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
      autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
1.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodpasture's syndrome, polyendocrinopathies, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain (CRD1) of the tumour LT-beta-R, which comprises a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 38
      disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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cardiovascular disorder; viral infection.
                                                                                                                                                                    Disclosure;
                                                                                                                                                                                      Nucleic acid encoding a TRID polypeptide, also referred to necrosis factor receptor 5, useful in the diagnosis, treatm
                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                        Wei Y,
                                                                                                                                                                                                                                                                                         WO200071150-A1
                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                  20-MAY-1999;
                                                                                                                                                                                                                                                               18-MAY-2000;
                                                                                                                                                                                                                                                                             30-NOV-2000
                                                                                                                                               (TNF) related apoptosis
                                                                                                                                                                                                                        Ruben
                                                                                                                                                                                of
                                                                                                                                                                   Fig 2; 285pp; English.
                                                                                                                                                      invention
                                                                                                                                                                                                                                                                2000WO-US13515
                                                                                                                                                                                cancer, autoimmune disorders and viral
                                                                                                                                                                                                                        , MS
                                                                                                                                                                                                                                                  99US-0135164
                                                                                                                                                                                                                        Gentz
                                                                                                                                                      describes the human TRID
                                                                                                                                                                                                                        RL,
                                                                                                                                                                                                                        Z.
                                                                                                                                               inducing ligand
                                                                                                                                                protein
(TRAIL)
                                                                                                                                                                                infection
                                                                                                                                                      (tumour necrosis
                                                                                                                                                                                       or
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polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autolumnune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The, antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases. associated with increased or decreased apoptotic cell death. The repolynucleotides, proteins, antibodies, agonists and antagonists cuseful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders. (c) discourage provention of: (d) cancer; (e) (b) autoimmune disorders;(c) diseases associated with increased apoptosis;(d) cardiovascular disorders;and(e) viral infection activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins intracellular domain, also referred to as tumour necrosis factor receptor 5 (TWRR-5 or TR5)). TRID has cytostatic, immunosuppress antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic nootropic, (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive neuroprotective, antiviral, antiinflammatory, anticonvuls with TRID in the exemplification necrosis factor receptor used antiinflammatory, anticonvulsant, of the present receptor without invention and

Sequence 415 AA;

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Matches
                     Query Match
Best Local
156 ARCQPHTRCE 165
                    Local
              10;
                     Similarity
               Conservative
                     5.1%;
               0;
                     Score
Pred.
             Mismatches
                     DB 22;
0.'049;
               0;
                             Length 415;
                Indels
              0;
              Gaps
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0

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В
      AAY20502
             RESULT
                                              80
AAY20502 standard;
                                  185
             7
                                 arcqphtrce 194
71
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ij

Protein;

AAY20502;

Human neurofilament-L mutant protein fragment

(first entry)

Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease;

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RESULT
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ID Ab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                        osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic; antirheumatic; antiarthritic; antilnflammation; immunomodulatory; tumour necrosis factor-related activation-induced cytokine; TRANCE; receptor activator of NF-kappaB ligand; RANK; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes peptides and peptide analogues which correspond in primary sequence to a binding loop of a tumour necrosis factor receptor (TNF-R) superfamily member. The compounds are especially designed from a binding loop of TNF-R p55. They are capable of inhibiting TNF binding to its cellular receptors and may be used to inhibit the biological activities of TNF. They may be used in treating TNF-associated conditions such as acute and chronic inflammatory
                                     08-FEB-2001
                                                                                                                                             periodontal
T cell prol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transdermal, transmucosal, pulmonary, subcutaneous, intravenous or intranuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present sequence represents an extracellular Cys-rich domain of TNF-R from present invention.
                                                                       WO200108699-A1
                                                                                                                                                        Paget's disease; metastatic bone disease; rheumatoid arthritis; periodontal disease; modulating dendritic cell maturation;
                                                                                                                                                                                                                                                                Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    responses, septic shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic reactions, immune complex disease, transplantation rejection and malaria. Administration is, e.g. oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Greene MI, Murali R,
                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                Human TNF-R extracellular Cys-rich domain TNF-R-rp SEQ ID
                                                                                                                                                                                                                                                                                                                                    30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                      AAB69194;
                                                                                                                                                                                                                                                                                                                                                                                                      AAB69194 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activities of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 VCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w compounds designed from a binding loop of a tumour necrosis ctor receptor - are capable of inhibiting the biological tivities of tumour necrosis factor, e.g., in treating inflammation autoimmune diseases
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                                                                                                                                         proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AA;
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                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.1%; 50.
100.0%; Pr
                                                                                                                                         CD40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 77; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                          77
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28-JUL-2000; 2000WO-US20510.

Misc-difference

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption inhibiting peptide analogues from the present invention have osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory and immunomodulatory activities, and are tumour necrosis factor (TNN)-related activation-induced cytokine (TRANCE)/ receptor activator of NF-kappaB ligand (RANK) inhibitors. The method is useful for treating diseases characterised by bone loss such as osteoporosis, Paget's disease, metastatic bone disease, rheumatoid arthritis or periodontal alsease, and modulating dendritic cell maturation. T cell proliferation and/or CD40 receptor systems. The present sequence represents an extracellular Cys-rich domain of a tumour necrosis factor recept the control of the control o
                                                                                                                                        multiple sclerosis; pernicious anaemia; Goodpasture's syndrome; autoimmune orchitis; myasthenia gravis; polyendocrinopathy; thyroiditis;
                                                                                                                                                                                         Crohn's disease; autoimmune gastritis; Still's disease; Behcet's disease; Sjogren's syndrome; ankylosing spondylitis; autoimmune uveitis; autoimmune lymphoproliferative syndrome; hyper IgM syndrome;
                                                                                                                                                                                                                                                                                           pre-ligand assembly domain; oligomerisation; inflammation; psoriasis;
periodic fever syndrome; sepsis syndrome; ulcerative colitis; ALPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aoki
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                                                                                                                                                                                                                                                                                                                                                                                            TNFR molecule LT-beta-R cysteine-rich domain #1 (CRD1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use
for
                                                                                                                                                                                                                                                                     adult respiratory distress syndrome; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                              TNFR superfamily; tumour necrosis factor receptor superfamily; PLAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU04498 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BARO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 VCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of peptides and peptide analogs which are {\tt TRANCE/RANK} inhibitors, inhibiting osteoclastogenesis and bone resorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention describes a method for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cthcellsdcppgteae
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                                                                 sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
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                                                                                                                                                                                                                                                                       LT-beta-R;
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This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift caused by, or associated with, an RNA molecule that has a frameshift caused by, or associated with, an RNA molecule that has a frameshift cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, continuities as another in an interpretation of the method disease, Down's syndrome, myotonic dystrophy, Huntington's disease, continuities type II and many others listed) or susceptibility to these disorders. The method callows a definitive diagnosis of Alzheimer's disease in living patients, ct. at an early stage. It is based on the observation that disease may be considered by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including conteins for proteins for proteins (beta-APP), the microtubule associated protein 2 (MAP2), neurofilament-i, neurofilament-i, neurofilament-i, neurofilament-i, neurofilament-i, controllament-i, neurofilament-i, neurofilament-i,
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diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-F, neurofilament-F; presentiin I; presentiin II; cellular tunnour antigen; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HWGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI. (UYRO-) UNIV ROTTERDAM ERASMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Figure 7; 258pp; English.
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                                                                                                                                                                                                                                                                                                                                                                       98WO-IB00705.
                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0043163.
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'-hac 7; Conserve
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                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                 W09845322-A2
                                                                                                                                                                                                                                                                                                                                                                    02-APR-1998;
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                                                                                                                                                                                      Synthetic
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by constitutions. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. The acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies contacting the amount of bound protein in the sample. The comparisor of downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by cerayme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed contacting in the contactor of the c
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                                                                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA, inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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                        Propionibacterium acnes immunogenic protein #26877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky YAW, Persing DH, Mitcham JL, Wang SS,
L'maisonneuve J, Zhang Y, Jen S, Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                           20-APR-2001; 2001WO-US12865
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Propionibacterium acnes immunogenic protein #19127.
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                                                                                                                                                                                                                                                                                         Skeiky YAW,
                                                                                                                                                         01-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and to produce other types of data and products dependent on DNA and amino acid sequences, ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 51103; 103pp; English.
                         Novel human diagnostic protein #20735.
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                                                                                                                                                                                                                                                                 Tang YT;
                                                                                                                                                                      30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                              31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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18-FEB-2002 (first entry)
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                                                                                                                  WO200175067-A2.
                                                                                           Homo sapiens.
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                                                                                                                                            11-OCT-2001.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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therefore treat P. acnes infections. The antibodies may also be used as
diagnostic agents for determining P. acnes presence, for example, by
SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelltis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA, inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
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                                                                                                                                      dermatological; osteopathic; neuroprotectant,
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100.0%; Pred. No.
:ive 0; Mismatch
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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e J, Zhang Y,
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                                                                                                                                                                                                             Propionibacterium acnes.
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Best Local Similarity
T; Conserve
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Propionibacterium acnes immunogenic protein #11038.
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tsspsar 81
                                                                                                                                                              WO200181581-A2.
                                                                                                                                                                                              01-NOV-2001
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                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 38490; 103pp; English.
                               Novel human diagnostic protein #8122.
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Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
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 (first entry)
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                                                               chromosome
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                                                                                                                                            WO200175067-A2
                                                                                                                Homo sapiens.
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 13-FEB-2002
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antignes, in the sample. The polypeptides may be used as antignes, in the sample. The polypeptides may be used as antignes, in the sample. The polypeptides may be used as antignes, in the sample. The polypeptides may be used as antignes, in the sample. The polypeptides may be used as antignes. These antibodies can be used to
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
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                                                                                                                       dermatological; osteopathic; neuroprotectant.
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100.0%; Pred. No. 23;
tive 0; Mismatches
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e J, Zhang Y, Jen S, Ca
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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Best Local Similarity
7; Conserve
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Drmanac RT, Liu C,
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N-PSDB; AAS69344.
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35 csrcppg 41
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                                                                             Homo sapiens.
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AAG55558
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                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                           Novel human diagnostic protein #1753.
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13-FEB-2002 (first entry)
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                                                                                        Homo sapiens.
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ABG05157
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990S-0148685.
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990S-0149768.
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99US-0140353.
99US-0140354.
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990S-0150884.
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99US-0143542.
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99US-0142920
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 22 - JUN - 1999;
23 - JUN - 1999;
24 - JUN - 1999;
25 - JUN - 1999;
29 - JUN - 1999;
30 - JUL - 1999;
01 - JUL - 1999;
06 - JUL - 1999;
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07 - JUL - 1999;
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  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 71260.
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22-MAY-15
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31-AUG-1999, 01-SEP-1999, 10-SEP-1999, 13-SEP-1999, 14-SEP-1999, 14-SEP-1999, 22-SEP-1999, 23-SEP-1999, 23-SEP-1999, 23-SEP-1999, 23-SEP-1999, 14-OCT-1999, 13-OCT-1999, 14-OCT-1999, 13-OCT-1999, 14-OCT-1999, 14-OCT-1999, 14-OCT-1999, 14-OCT-1999, 14-OCT-1999, 13-OCT-1999, 23-OCT-1999, 23-OC
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; Query Match 3.6%; Score 7; DB 21; Length 211; Best Local Similarity 100.0%; Pred. No. 41; Matches 7; Conservative 0; Mismatches 0; Indels

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Gaps

176 TAQSDTT 182 ò

Search completed: October 4, 2002, 10:16:32 Job time: 245 sec

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NAME: HALEY, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B191
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 596-9000
TELEPAX: (212) 596-9000
TELEX: 14-8367
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-505-606-1
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(without alignments)
371.571 Million cell updates/sec
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/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-129-129-6
US-08-453-924-8
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US-09-373-324A-6
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US-09-372-435-6
US-09-137-016-2
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US-09-146-950-20 US-08-113-341-13 US-08-113-825-1 US-08-199-842-1 US-08-906-769-178 US-08-906-769-178 US-09-004-731-77 US-09-012-431-178 US-09-012-632-178 US-09-012-632-178 US-09-012-632-178 US-08-906-613-178 US-08-906-613-178 US-08-906-613-178 US-08-9146-950-2 US-08-146-950-2 US-08-679-493A-215 US-09-146-950-1 US-08-679-493A-215 US-08-679-493A-215 US-09-146-950-1 US-08-178-178-178-178-178-178-178-178-178-17	ALIGNMENTS	ication US/08505606 MINION WINDON WINDON WINDON WINDON WINTON W
1159 4 4 1191 4 4 1197 2 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		NX: NING, Jeffrey L NAING, Jeffrey L NAING, Jeffrey L NAIN, Christoph NAAN, Paula S. NAAN, SOLUBLE LY CON: ANTI-LYMPH CON: THERAPEUTI CON: ANTI-LYMPH A Avenue of the A A Avenue of the A A A A A A A A A A A A A A A A A A A
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Matches 77; Conservative
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CITY: ROC
STATE: MD
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TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
TITLE OF INVENTION: USES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                        ;
0
  Length 197;
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                                        Indels
100.0%; Score 197; DB 2; I
100.0%; Pred. No. 7.8e-198;
ive 0; Mismatches 0;
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,545
FILING DATE: 30-MAY-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: COTUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REFEROMMUNICATION NUMBER: 009113-0004-999
TELEPOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEHERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Mural1, Ramachandran
APPLICANT: Takasaki, Wataru
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08866545 Patent No. 6265535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: No. 6265535e
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                          181 TICKNPLEPLPPEMSGT 197
                                                                                                                                                                                                                                                                                                                              181 TTCKNPLEPLPPEMSGT 197
                      Best Local Similarity 100. Matches 197; Conservative
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Best Local Similarity
                    Similarity
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US-07-973-324A-6
Sequence 6. Application US/07973324A
Sequence 6. Application US/07973324A
Setent No. 5460952
GENERAL INFORMATION:
APPLICANT: IV. Su-May
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
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100.0%; Pred. No. 0.017;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                  APPLICANT: WEL, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTY, REINER
APPLICANT: GENTY, REINER
APPLICANT: GENTY, REINER
APPLICANT: GENTY, RECEPTOR
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NOMBER OF SEQUENCES:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version:#1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISEE: HUMAN GENOME SCIENCES, INC. 19410 KEY WEST AVENUE ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                                  Sequence 6, Application US/09006353A Patent No. 6261801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIF: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
RECISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                         112 CTHCELLSDCPPGTEAE 128
                                                                                                             61 CTHCELLSDCPPGTEAE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.1
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 ARCQPHTRCE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 ARCQPHTRCE 194
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Gaps

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APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Liu, Ming-Tsair
ITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE
TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
                                                                                                                                                                                                                                                                                                                                                          Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Marshall, O'Toole, Gerstein, Murray
233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENY APPLICATION DATA:
RAPLICATION NUMBER: US/09/072,435
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                      DB 1;
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERRUCE/DOCKET NUMBER: 38,153
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-072-435-6; Sequence 6, Application US/09072435; Patent No. 6215051
                         REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                       LENGTH: 437 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-343-380-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-072-435-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
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Patent No. 5712112
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
COUWTRY: United States of America
ZIP: 6060-640.2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25.
CURRENT APPLICATION DATA:
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 7; DB 1;
100.0%; Pred. No. 24;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/973,324A FILING DATE: 04-NOV-1992 CLASSIFICATION: 435
                                                                                                         STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/343,380 FILING DATE: 22-NOV-1994 CLASSIFICATION: 435
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APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 437 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDALL
STREET: 65.0
-mv: Chicago
                                                                                    Chicago
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US-08-343-380-6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Was.....
STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                              STATE: D. C. COUNTRY: U.S.A. ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 TSSPSA 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-08-137-016-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6288302

TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
APPLICANT: Chan, Ming-Tsair
IITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                               Gaps
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  Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: 111inois
COUTRY: United States of America
21P: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,917A
Query Match 3.6%; Score 7; DB 4 Best Local Similarity 100.0%; Pred. No. 24; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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3.6%; Score 7; [
Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                        Sequence 6, Application US/09072917A Patent No. 6288302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-08-137-016-2
; Sequence 2, Application US/08137016
; Sequence 2, Application US/08137016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-072-917A-6
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                124 GTEAELK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 GTEAELK 130
                                                                                                                       90 GTEAELK 96
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APPLICANT: WILE Geoffey
APPLICANT: TAIN, weasign
TITLE OF INVESTION: Synthetic CDM52 (Campath-1) Peptide Antigen
ITTLE OF INVESTION: Synthetic CDM52 (Campath-1) Peptide Antigen
OUNDESCORES: 14
CONGRESS: 801E-071E, 555 Thitteenth St., N.W
CONGRESS: 101E-071E, 10
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Gaps

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RESULT 11
US-08-137-016-5
US-08-137-016-5
Sequence 5, Application US/08137016
Partent No. 5444999
GENERAL INFORMATION:
APPLICANT: HALE, Geoffrey
APPLICANT: TIA, Meng-0i
TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Nurs
ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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STATE: D. C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,016
FILING DATE: 05-OCT-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,016
FILING DATE: 16-APR-1992
PRIOR APPLICATION NUMBER: US/08/137,016
FILING DATE: 16-APR-1992
RIUNG DATE: 16-APR-1992
RIUNG DATE: 16-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: EINST, BATCHARTON:
NAME: EINST, BATCHARTON:
NAME: EINST, BATCHARTON:
NAME: REGISTRATION NUMBER: 30,377
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.0%; Score 6; DB 1.
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches
             30,377
                                                  REFERENCE/DOCKET NUMBER: 17
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                        single
linear
7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 TSSPSA 156
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US-08-137-016-4
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| Patent No. 549499 |
| GENERAL INFORMATION: SAPPLICANT: HALE, Geoffrey |
| APPLICANT: TONE, Masahide |
| APPLICANT: TONE, Masahide |
| APPLICANT: TAIA, Meng-Oi |
| TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen |
| WUMBER OF SEQUENCES: 14 CORRESSEE: Rothwell, Figg, Ernst & Kurz |
| CORRESPONDENCE ADDRESSE: Application |
| STREET: Suite 701-E, 555 Thirteenth St., N.W |
| COUNTRY: U.S.A. |
| STATE: D. C. |
| COUNTRY: U.S.A. |
| COMPUTER: EADABLE FORM: |
| MEDIUM TYPE: Floppy disk |
| COMPUTER: BEN PC Compatible |
| COMPUTER: Patentin Release #1.0, Version #1.25 |
| CURRATING SYSTEM: PATENT APPLICATION DATA: |
| CONTROL MANDAN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 14;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                               APPLICATION NUMBER: US/08/137,016
FILING DATE: 05-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB 92/00705
FILING DATE: 16-APR-1992
PRIOR APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
ATORNEY/AGENT INFORMATION:
NAME: Ernst, Barbar G,
REGISTRATION NUMBER: 30,377
- REFERENCE/DOCKET NUMBER: 1769-116
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 12
Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB 92/00705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/137,016 FILING DATE: 05-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (202)783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 amino acids
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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8 TSSPSA 13
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US-08-137-016-3
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Sequence 7, Application US/08137016
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8 TSSPSA 13
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US-07-826-928A-11
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                                                                                                                                                                                                                                                 Sequence 6, Application US/08137016
Patent No. 5494999
GENERAL INFORMATION:
APPLICANT: TONE, Masshide
APPLICANT: TONE, Masshide
APPLICANT: XIA, Meng-Qi
TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
NUMBER OF SEQUENCES: 14
CORRESPONENCE ADDRESS:
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                                                     Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,016

FILING DATE: 05-OCT-1993

PRIOR APPLICATION NUMBER: WO PCT/GB 92/00705

FILING DATE: 16-APR-1992

PRIOR APPLICATION NUMBER: GB 91 08056.4

FILING DATE: 16-APR-91

ATTORNEY/AGENT INFORMATION:

NAME: Ernst, Barbara G:

RESISTRATION NUMBER: 30,377

RESISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1768-116
                                                                                                                                                                                                                                                                                                                                                                                                                          E: Rothwell, Figg, Ernst & Kurz
Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 14; ive 0; Mismatches
                                                   Query Match 3.0%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEPAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D. C.
: U.S.A.
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Best Local Similarity
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MOLECULE TYPE: pe
                                                                                                                              151 TSSPSA 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE:
US-08-137-016-6
                                                                                                                                                                                                                      RESULT 12
US-08-137-016-6
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US-08-137-016-5
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US-08-137-016-7
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APPLICANT: ANGERSON, Leslie D.
APPLICANT: Anderson, Leslie D.
APPLICANT: Cook, James A.
APPLICANT: David, Gary S.
APPLICANT: Hochschwender, Susan M.
APPLICANT: Smith, Michele C.
APPLICANT: Stemmer, Willem P.
TITLE OF INVENTION: METHOD OF IMMOBILIZING AND CROSS LINKING
TITLE OF INVENTION: PROTEINS AND OTHER MOLECULES AND USES THEREOF
CORRESPONDENCE ADDRESS:
APPLICANT: HALE, Geoffrey
APPLICANT: TONE, Masahide
APPLICANT: XIA, Meng-Qi
TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                   COMPUTAT: U.S.A.

CONDUTER: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPACH
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/137,016
FILING DATE: US-08/137,016
FILING DATE: 16-APR-1992
PRIOR APPLICATION NUMBER: WO PCT/GB 92/00705
FILING DATE: 16-APR-991
RYCH APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: Enrst, Barbara G. 377
REGISTRATION NUMBER: 30,377
REGISTRATION NUMBER: 30,377
REGISTRATION NUMBER: 30,377
                                                                                                                                                                        ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 6; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              red. No. 15;
Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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Best Local Similarity 100.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                              STATE: D. C. COUNTRY: U.S.A.
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0; Gaps

Length 40; 0; Indels

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FILING DATE: 08-APR-1992

ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
RESISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 203424/T7016(C)
TELECHANE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELEFAX: (202) 861-3000
TELEFAX: 6714627CUSH
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                Score 6; DB 1; Pred. No. 31; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: October 4, 2002, 10:16:52 Job time: 220 sec
                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-129-129-6
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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APPLICANT: DE SILVA, Jacqueline
APPLICANT: DE SILVA, Sichard
APPLICANT: SAFFORD, Richard
APPLICANT: HUGHSK, Stephen Glyn
TITLE OF INVENTION: CONTROLLING LIPID BIOSYNTHESIS IN SEEDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 23;
                                                                                                                                                                                                    SOFTWARENT STATEM.
SOFTWARENT APPLICATION DATA:
APPLICATION NAME: US/07/826,928A
FILING DATE: 19920124
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: Murphy, Richard B.
REGISTRATION NUMBER: 35,296
REGISTRATION NUMBER: 35,296
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1276-1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.0%; Score 6; DB 1;
100.0%; Pred. No. 19;
iive 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91303098.7
FILLING DATE: 09-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/129,129
FILING DATE: 18-JAN-1994
CLASSIFICATION: 800
ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                    ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08129129
Patent No. 5767363
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 317-276-3589
TELEFAX: 317-276-1294
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.0
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D. C. COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                       USA
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Search time 19.61 Seconds (without alignments) 965.303 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. pir1:* pir2:* pir3:* pir4:* Database :

Post-processing: Listing first 45 summaries

seq length: 0 seq length: 2000000000

Minimum DB: Maximum DB:

exo-poly-alpha-gal hypothetical prote hypothetical prote GPI-anchored epidi hypothetical prote H+-transporting AT probable atpE prot hypothetical prote molybdate-binding avermectin B 5-0-m C5-0-methyltransfe hypothetical prote pyruvate dehydroge alpha-amylase 3E alpha-amylase (EC conserved hypothet nitrogenase molybd hypothetical prote probable Glu-tRNA(adenylosuccinate s petH protein - Syn hypothetical prote prote tumor necrosis fac hypothetical prote probable pilln PA4 probable 5'-nucleo prote hypothetical hypothetical acyl carrier Description SUMMARIES JC6531 144579 686263 T00342 JC71346 JC7134 G82241 G69075 T18904 T18904 A13295 A82447 S72635 A89959 S30855 S18766 D42194 D90762 E97642 AG2865 H97132 C83134 F36914 DB Length 61 Query Match 1 777777777779999999999 Score Result

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I54182 tumor necrosis fact C;Species: Homo sap C;Date: 24-May-1996 C;Accession: I54182	is fac omo sa ay-199 IS418	factor sapier 1996 #8	actor receptor sapiens (man) 996 #sequence 182	n)	2- rev	crosis factor receptor 2-related protein - human s: Homo sapiens (man) 24-May-1996 #sequence_revision 24-May-1996 #text_change 17 ion: I54182	17-Mar-2000
R; Baens, M.; Genomics 16, A:Title: Cons	M.; Chaffanet, M. 16, 214-218, 1993 Construction and	fane 218,	1993 1993 and		ssi	; Cassiman, J.J.; Van den Berghe, H.; Ma ; evaluation of a hncDNA library of human	H.; Marynen, P. buman 12b transcribed sed
	number 15418 elimir	32 III	54182; MUID:	MU	ID:	/EMBL/DDBJ	
	Lype: mana 1-435 <re erences: G :LTBR</re 	KRE KRE S: GI	S> B:L042	70;		NID:9339761; PIDN:AAA36757.1; PID:9	PID:g339762
A;Cross-references: GDB:123019; A;Map position: 12p13.3-12p13. C;Superfamily: tumor necrosis	rences on: 15 y: tum	ces: GI 12p13, tumor	GDB:1230195; 3.3-12p13.1 necrosis fa	019 13. is	1 fac	5; OMIM:600979 1 factor receptor type 1; NGF receptor	repeat homology
Query Match Best Local Matches 19	Simi 7;	larii	vat	100.0%; 100.0%; ive	** ***	; Score 197; DB 2; Length 435; ; Pred. No. 1.2e-204; 0; Mismatches 0; Indels	0; Gaps 0;

hypothetical protein CAC1887 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: H97132
R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Batteriol. 183, 4823-4838, 2001 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 120 147 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180 207 9 87 148 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENGGLVEAAPGTAQSD 181 TTCKNPLEPLPPEMSGT 197 208 TTCKNPLEPLPPEMSGT 224 28 61 121 a qq δ q ò ò q

us-09-299-139a-1.rpr

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Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
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| 138 AAWALEC 144
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                             169 LVEAAPG 175
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A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium ClA; Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97132
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <KUR>
A;Cross_references: GB.AE001437; PIDN:AAK79851.1; PID:g15024867; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A.Reference number: A82950; MUID:2043737
A.Reference number: A82950; MUID:20437337
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-189 < STO>
A.Cross-references: GB:AE004825; GB:AE004091; NID:99950284; PIDN:AAG07473.1; GSPDB:GN001
A.Status: A.Status: Panda
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D. Bacteriol. 175, 3031-3042, 1993
A;Title: Characterization of Rhodobacter capsulatus genes encoding a molybdenum transpor A;Reference number: A36914; MUID:93259949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable pilin PA4086 [imported] - Pseudomonas aeruginosa (strain PA01)
C.Species: Pseudomonas aeruginosa
C.Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molybdate-binding protein homolog MopA - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
C;Accession: F36914
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**Residues: 1-265 G/ANA **

**A;Residues: 1-265 G/ANA **

**A;Note: sequence extracted from NCBI backbone (NCBIN:131915, NCBIP:131921)

C;Superfamily: molybdate-binding protein
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100.0%; Pred. No. 8.4;
ive 0; Mismatches
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100.0%; Pred. No. 18;
Live 0; Mismatches
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100.0%; Pred. No. 14;
iive 0; Mismatches
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Matches 7; Conservative
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Les 7; Conservative
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A; Status: preliminary
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avermectin B 5-0-methyltransferase (EC 2.1.1..) - Streptomyces "avermitilis" C; Species: Streptomyces "avermitilis" C; Species: Streptomyces "avermitilis" C; Species: O5-Dec-1998 #sequence_revision O5-Dec-1998 #text_change 16-Jul-1999 C; Accession: JG6531 R: Ikeda, H: Wang, L.R.; Ohta, T.; Inokoshi, J.; Omura, S. Gene 206, 175-180, 1998 A; Title: Cloning of the gene encoding avermectin B 5-0-methyltransferase in avermectin A; Reference number: JC6531; MUID:98137789
                                                                                                                                                                                                                                                                 A.Accession: JC6531
A.Moleoule type: DNA
A.Residues: 1-283 <IKE>
A.Experimental source: wild type K139
C.Coment: This enzyme catalyzes the methylation of the hydroxyl group at the C5 post
A.Genetics:
A.Gene: avep
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C;Species: 0.2-Mar-2001 #sequence_revision 0.2-Mar-2001 #text_change 31-Dec-2001
C;Accession: G86Ex, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
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C;Genetics:
A;Note: aveD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C5-0-methyltransferase [imported] - Streptomyces avermitilis
C;Species: Streptomyces avermitilis
C;Species: Streptomyces avermitilis
C;Bacession: T44579
R;Ikeda, H.; Nonomiya, T.; Usami, M.; Ohta, T.; Omura, S.
Proc. Natl. Acad. Sci. U.S.A. 96, 9509-9514, 1999
A;Title: Organization of the blosynthetic gene cluster for the polyketide an
A;Reference number: 222766, MUID:99380548
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A,Molecule type: DNA
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100.0%; Pred. No. 20;
iive 0; Mismatches
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100.0%; Pred. No. 20;
tive 0; Mismatches
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C.Keywords: methyltransferase
F;68-172/Domain: bloc homology <BIOC>
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A;Residues: 1.449 <HEI>
A;Cross-references: GB:AE004191; GB:AE003852; NID:99655568; PIDN:AAF94267.1; GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha-amylase (EC 3.2.1.1) isozyme III - rice
NyAlternate names: 1.4-gulcan glucanohydrolase III
C;Species: Oryza sativa (rice)
C;Date: Our Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C;Accession: JC7138; Pc7040
C;Accession: JC7138; Pc7040
R;Abc, R; Yoshida, R; Aoyaqi, M; Kasahara, S; Ichishima, E; Nakajima, T.
Biosci. Blotechnol. Blochem. 63, 1329-1335, 1999
A;Title: Characterization of chimeric enzymes constructed between two distinct alpha-A;Reference number: JC7137; MUID:99430781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 246-253 -4882>
C;Comment: This enzyme datalyzes the hydrolysis of internal alpha-glucosidic linkages
is important in germinating seeds and presenting as multiple isoforms.
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers Li. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein VC1108 [imported] – Vibrio cholerae (strain N16961 ser
                                                                                        PIDN: AAA33896.1; PID:g169773 homology
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A;Map position: 1
C;Superfamily: Haemophilus influenzae conserved hypothetical protein HI1590
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Reywords: calcium binding; germination; glycosidase; hydrolase;
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                                         A; Molecule type: DNA
A; Residues: 1-437 <HUA>
A; Cross-references: GB:M59352; GB:M36985; NID:g169772;
C; Superfamily: wheat alpha-amylase; alpha-amylase core
F;171-315/Domain: alpha-amylase core homology <AMY>
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100.0%; Pred. No. 28;
ive 0; Mismatches
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100.0%; Pre
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Matches 7; Conserv
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A; Residues: 1-437 <ABE>
A; Accession: PC7040
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            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                 90 GTEAELK 96
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90 GTEAELK 96
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C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 21-Jan-2000
C;Accession: JT0948
R;Huang, N.; Kolzumi, N.; Reinl, S.; Rodriguez, R.L.
Nucleic Acids Res. 18, 7007-7014, 1990
A;Title: Structural organization and differential expression of rice alpha-amylase genes A;Reference number: JT0945; MUID:91088278
A;Accession: JT0946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rigrof, C.P.; Winning, B.M.; Scaysbrook, T.P.; Hill, S.A.; Leaver, C.J.
Plant Physiol. 108, 1623-1629, 1995
Affitle: Witochondrial pyruvate dehydrogenase. Molecular cloning of the El alpha subunit
A;Reference number: 215993; MUID:95388769
A;Accession: T07372
ansen, N.F.; Hughes, B.; Huizar, L.
Mature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Aturhors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
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A; Residues: 1.391 <GRO>
A; Cross-references: EMBL: Z26949; NID:g473168; PIDN:CAA81558.1; PID:g473169
A; Experimental source: Cv. Desiree; tissue type leaf
C; Genetics:
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100.0%; Pred. No. 22;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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A; Molecule type: DNA
A; Residues: 1-328 <STO>
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C; Complex: heterot
C; Function:
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probable Glu-tRNA(Gln) amidotransferase chain B - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: OS-Nov-1999 #text_change 21-Jan-2000 C; Date: OS-Nov-1999 #text_change 21-Jan-2000 C; Date: OS-Nov-1999 #text_change 21-Jan-2000 C; Date: OS-Nov-1999 #text_change 21-Jan-2000 R; Murphy, L; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1999 A; Reference number: 221589 A; Accession: T35817 A; Refatus: preliminary; translated from GB/EMBL/DDBJ A; Accession: T35817 A; Accession: T35817 A; Mesidues: 1-504 cMUR> A; Residues: 1-504 cMUR> A; Residues: 1-504 cMUR> A; Residues: EMBL:AL035569; PIDN:CAB37577.1; GSPDB:GN00070; SCOEDB:SCBD9.13 A; Cross-references: EMBL:AL035569; PIDN:CAB37577.1; GSPDB:GN00070; Marchian 1890 A; A; Cross-references: EMBL:AL035569; PIDN:CAB37577.1; GSPDB:GN00070; Marchian 1890 A; Cross-references: EMBL:AL035569; PIDN:CAB375
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Best Local Similarity 100.0
Matches 7; Conservative
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C;Superfamily: PET112 protein
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Best Local Similarity
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266 MGLEEIA 272
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18 DPVMGLE 24
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A; Map position: I
C; Keywords: ligase
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A;Reference number: 219042
A;Reference number: 218094
A;Accession: T18904
A;Accession: T18904
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-474 < WHIL>
A;Cross-references: EMBL:569716; PIDN:CAA93527.1; GSPDB:GN00028; CESP:C04B4.2
A;Experimental source: clone C04B4
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T18904
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100.0%; Pred. No. 30;
iive 0; Mismatches
                                         3.6%; Score 7; DB 2
100.0%; Pred. No. 29;
Live 0; Mismatches
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ive 0; Mismatches
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C;Superfamily: dinitrogenase beta chain
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A;Gene: CESP:C04B4.2
A;Map position: X
A;Introns: 67/3; 161/2; 207/3; 435/1
Ouery Match
Best Local Similarity 100،۰۰
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448 EYYEPQH 454
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"Georgias Brucella melitensis (5.3.4.4) [imported] - Brucella melitensis (strain 16M c) Species: Brucella melitensis (5.5pecies: Brucella melitensis Brucella Brucella melitensis Brucella 
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-520 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51532.1; PID:g17982249; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
                                                                                                                                             Gaps
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100.0%; Pred. No. 33;
tive 0; Mismatches
             3.6%; Score 7; DB 2
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tive 0; Mismatches
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ACP4_CUPLA ACP1_CUPLA NIU2_RHOCA ACP3_CUPLA PPIB_BACSU ACP1_HORVU NDK1_DRYSA NDK_ARCFU ACP2_ARATH RAOS_ORYSA RSVR_COTJA ACP3_ARATH

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summaries

Post-processing: Listing first 45 Minimum DB seq length: 0 Maximum DB seq length: 200000000

SUMMARIES

		Description	P36941 homo sapien	3284 mus m	stre	Q08385 rhodobacter	P52903 solanum tub	P52004 brucella ab	P27934 oryza sativ	methan	P95296 methanobact	Q9z578 streptomyce		P32634 saccharomyc	P31358 homo sapien	P32040 synechococc	P45828 mycobacteri	Q10598 mycobacteri	O88870 mus musculu		-	-	051351 borrelia bu		O78414 guillardia	P15543 hordeum vul			_	P08971 brassica na	P07088 brassica ca	P45279 haemophilus	~	1829 arabido	P52412 cuphea lanc
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200		:	TNR3_H	\mathbb{R}^{3}	rΛ	MOPA_R	ODPA_SOLTU	PURA_B	AM3E_O	NIFK_M	NIFK	GATB_STRCO	E1_R	YEW2_YEAST	CD52_HUMAN	YPH2_SYNP2	ATPL_MYCLE	ATPL_MYCTU	VMD2_MOUSE	THIO_CLOLI	THIO_E	YQCD_BACSU	RL7_BORBU	ACP2_HORVU	RK12_GUITH	ACP3_HORVU	ACP1_BRANA	ACP2_BRANA	ACP3_BRANA	P5_B	ACP_BRACM	CB_H	ACP1_C	P1_A	ACP2_CUPLA
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-i - SUBCELLULAR LOCATION: Type I membrane protein.
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SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC 700294 / Serotype M1;
MEDLINE-21192684; PubMed=11296296;
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100.0%; Pre
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MGD; MGI:104675; Ltbr.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
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                                                                                                      EMBL; U29173; AAA68964.1; -. EMBL; L38423; AAB00846.1; -. EMBL; U30798; AAA81334.1; -.
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415 AA;
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-1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN IMMUNE DEVELOPMENT.
                                                                                                                                                                                                                                                                     61 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 120
                                                                                                                                                                                                                                                                               88 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 147
                                                                                                                                                                                                                                                                                                          121 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CVB; TISSUB-Lung; MEDIAG-7594541; MEDIAE-9602804; PubMed-7594541; Force W.R., Walter B.N., Hesslon C., Tizard R., Kozak C.A., Browning J.L., Ware C.F.; "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding, and expression."; Immunol. 155:5280-5288(1995).
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                         28 SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 87
                                                                                                                                                                                                                               SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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MEDLINE-96163885; PubMed-8586432;
Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
                                                                                                                                                                                           Length 435,
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624626E6022F656F CRC64;
 CYTOPLASMIC (POTENTIAL)
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100.0%; Pred. No. 8.3e-202;
ive 0; Mismatches 0;
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Lymphotoxin-beta receptor precursor.
LTBR OR TNFCR OR TNFRSF3.
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                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
16-0CT-2001 (Rel. 40, Last ann
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208 TTCKNPLEPLPPEMSGT 224
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Best Local Similarity 100.
Matches 197; Conservative
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N-LINKED (GLCNAC. . .) (POTENTIAL).
29B326A566AEF661 CRC64;
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Pred. No. 0.0076;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00652; TWFR_NGFR_1; 2.
PROSITE; PS50605; TWFR_NGFR_2; 3.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
1 30 POTENTIAL.
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                                                                                                                                Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Olan Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 33303 / B10;
STRAIN-ATCC 33303 / B10;
STRAIN-ATCC 33259949; Pubmed-8491722;
Wang G., Angermueller S., Klipp W.;
"Characterization of Rhodobacter capsulatus genes encoding a molybdenum transport system and putative molybdenum-pterin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initiation factor; Protein blosynthesis; Complete proteome.
SEQUENCE 176 AA; 20053 MW; FD3247FB6C9D5919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1994 (Rel. 30, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Molybdenum-pterin binding protein mopA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                      -!- SUBUNT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE IF-3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.6%; Score 7; DB 1
100.0%; Pred. No. 5.6
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 175:3031-3042(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE006531; AAK33741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1994 (Rel. 30, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001288; IF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD002880; IF3; 1. PROSITE; PS00938; IF3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00707; IF3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 QPQAVPP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 QPQAVPP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOPA_RHOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Millar A.H., Knorpp C., Leaver C.J., Hill S.A.;
"Plant mitochondrial pyruvate dehydrogenase complex: purification and identification of catalytic components in potato.";
Biochem. J. 334:571-576(1998).
-!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1), DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pyruvate dehydrogenase El component alpha subunit, mitochondrial precursor (EC 1.24.1) (PDHE1-A).
Solanum tuberosum (Potato).
Enkaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae: euasterids I; Solanales; Solanaceae; Solanum.
NUBL_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grof C.P., Winning B.M., Scaysbrook T.P., Hill S.A., Leaver C.J.; "Mitochondrial pyruvate dehydrogenase. Molecular cloning of the El alpha subunit and expression analysis."; Plant Physiol. 108:1623-1629(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acetyldihydrolipoamide + CO(2).
--- COFACTOR: THIAMINE PYROPHOSPHATE.
--- ENZYME REGULATION: E1 ACTIVITY IS REGULATED BY PHOSPHORYLATION (INACTIVATION) AND DEPHOSPHORYLATION (ACTIVATION) OF THE ALPHA
                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT (BY SÍMILARITY).
SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS (BY
                                                                                                                                                                                Length 265;
                                                                                                                                                                                                                       Indels
                                                                                                                       7EB89FC938CAF326 CRC64;

    -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                DB 1;
. 8;
                                                                                                                                                                              Score 7; DB 1; Pred. No. 8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                  MOP-LIKE.
                                                                                                      MOP-LIKE
                                                                                                                                                                3.6%; Scur-
100.0%; Pred
0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. DESIREE; TISSUE-Leaf;
MEDLINE-95388769; PubMed-7659754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. ROMANO; TISSUE-Tuber;
MEDLINE-98399821; PubMed-9729464;
EMBL, L06254; AAA71912.1; -.
InterPro; IPR003725; Mode.
Pfam; PF02573; Mode; 1.
Transport; Molybdenum; Repeat.
REPEAT 125 MOF
REPEAT 193 265 MOF
                                                                                                                       265 AA; 27119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z26949; CAA81558.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001017; E1_dh.
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
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SEQUENCE OF 27-42.
                                                                                                                                                                                                                                                            169 LVEAAPG 175
                                                                                                                                                                                                                                                                                                 66 LVEAAPG 72
                                                                                                                                                                                                                                                                                                                                                                                                 ODPA_SOLTU
P52903;
                                                                                                                       SEQUENCE
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Gaps

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Indels

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Mismatches Pred. No.

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100.08;

12;

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Conservative
    Best Local Similarity
                                                                                                                                                                                                           AM3E_ORYSA
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ACT_SITE
CA_BIND
CA_BIND
SEQUENCE
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                       Matches
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                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished observations (NOV-1999).
-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE DE NOVO PATHWAY OF PURINE NUCLEOTIDE BIOSYNTHESIS.
-!- CATALYTIC ACTIVITY: GTP + IMP + L-aspartate = GDP + phosphate +
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- PATHWAY: FIRST COMMITTED STEP IN AMP BIOSYNTHESIS.
Pfam; PF00676; El_dehydrog; 1.
Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate; Phosphorylation; Mitochondrion; Transit peptide.
TRANSIT MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XKYVRHIEEL -> SNMSAISKS (IN REF. 1).
                                                                                  PYRUVATE DEHYDROGENASE E1 COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                              ;
                                                                                                                                                                                      Length 391;
                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tatum F.M., Steckelberg M.A.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                       ALPHA SUBUNIT.
F9110B374B022F0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F443CFAE8D10EE75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION OF A PROBABLE C-TERMINAL FRAMESHIFT.
                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTY: PRO01114; Adenylsucc_synt.
Pfam; PF00709; Adenylsucc_synt; 1.
ProDom; PD001188; Adenylsucc_synt; 1.
PROSTIE; PS00513; ADENYLOSUCCIN_SYN_2; 1.
Purine biosynthesis; Ligase; GTP-binding.
NP_BIND 12 18
                                                                                                                                                                                                                                                                                                                                                                                                                402 AA
                                                                                                                                                                                    3.6%; Score 7; DB 1
100.0%; Pred. No. 11;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last seq
16-0CT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43919 MW;
                                                                                                                           43228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L43054; AAA75455.1; -.
HSSP; P12283; 1ADE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ADSS) (AMPSase) (Fragment)
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brucellaceae; Brucella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adenylosuccinate.
                                                                                                                           391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 AA;
                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                           332 TEAELKD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brucella abortus
                                                                                                                                                                                                                                                                       125 TEAELKD 131
                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=2308;
                                                                                                                                                                                                                                                                                                                                                                                                                FURA_BRUAB
P52004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michoud K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
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                                                                                                                           SEQUENCE
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DB 1; Length 402;

3.6%; Score 7;

Query Match

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                                                                                                                                                                                                              15-DEC-1992 (Rel. 23, Last sequence update)
Alpha-anylase isozyme 3E precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. JAPONICA M202; TISSUE-Etiolated leaf;
MEDLINE-91088278; PubMed-2263460;
MEDLINE-9108078; No Roizumi N., Realini S., Rodriguez R.L.;
"Structural organization and differential expression of rice alpha-
                                                                                                                                                                                                                                                                                                                                     AMYI.4 OR AMYJE.
Orgza sativa (Rice).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL. SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000461; Alpha_amylase.
Pfam: PF00128; alpha-amylase; 1.
Pfam: PF00128; alpha-amylase; 1.
Multigene family. Signal; Signal; Signal.
Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amylase genes.";
Nucleic Acids Res. 18:7007-7014(1990).
-!- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
A; COE8276CCEA16602 CRC64;
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100.0%; Pred. No. 12;
iive 0; Mismatches
                                                                                                                                                                 437 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M59352; AAA33896.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; JT0946; JT0946.
HSSP; P04063; IAVA.
Mendel; 9691; ORYsa;Amyl;4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48707
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                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
437
204
312
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175
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥
                              ||||||||
|75 MGLEEIA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GERMINATION.
81 MGLEEIA 87
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027606;

RESULT 8 NIFK_METTH

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459 AA.
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      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X87971; CAA61220.1; -. HSSP; P11347; 1MIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
                                                                                                                                                                                                     Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=79929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subunit B).
GATB OR SC8D9.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 EYYEPQH 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 EYYEPQH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATB_STRCO
    NIFK_METTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
GATB_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            deltah: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
I. FUNCTION: THE KEY ENZYMATIC REACTIONS IN NITROGEN FIXATION ARE
CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.
I. CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP
= 8 oxidized ferredoxin + 2 NH(3) + 16 ADP + 16 phosphate.
I. SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
30-32 FE, 2 MO, AND INORGANIC SULFUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                        30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Nitrogenase molybdenum-iron protein beta chain (EC 1.18.6.1)
(Nitrogenase component I) (Dinitrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00148; oxidored_nitro; 1.
PROSITE; PS00090; NITROGENASE_1_2; 1.
PROSITE; PS00699; NITROGENASE_1_1; 1.
Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.6%; Score 7; DB 1; Length 459;
100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 AA; 51489 MW; F2CB731BCC675AC9 CRC64;
                                                                                                                                         459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000318; Nitrognse_comp1.
InterPro; IPR000510; Oxidored_nitrognse_1.
                                                                                                                                                                                                                                                                                               Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=DELTA H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000916; AAB86038.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                    Methanothermobacter.
NCBL_TaxID=145262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 459 AA;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
124 GTEAELK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 EYYEPQH 454
                                     90 GTEAELK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 EYYEPQH 28
                                                                                                                                         NIFK_METTH
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                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.-) (Glu-ADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                           Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133)
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murphy L., Harris D., Bentley S.D., Parkhill J., Barrell B.G.,
Rajandream M.A.;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Nitrogenase molypdenum-iron protein beta chain (EC 1.18.6.1)
(Nitrogenase component I) (Dinitrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00148; oxidored_nitro; 1.
PROSITE; PS00090; NITROGENASE_1_2; 1.
PROSITE; PS00699; NITROGENASE_1_1; 1.
Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
SEQUENCE 459 As; 51158 MW; 04F03EA9CB3E9E37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                  Hochheimer A.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.6%; Score 7; DB 1;
100.0%; Pred. No. 13;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000318; Nitrognse_compl.
InterPro; IPR000510; Oxidored_nitrognse_1.
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RESULT
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Lunchitted (101-1994) to the EMBL/GenBank/DDBJ databases.

Lunchitted (101-1994) to the EMBL/GenBank/DDBJ databases.

Lunchitted (101-1994) to the EMBL/GenBank/DDBJ databases.

CIT ON TRANSITION: MAY ACT AS A NEGATIVE REGULATOR OF ENTRY INTO MITOSIS

CONSET OF MITOSIS. ITS ACTIVITY INTREASES DURING S AND G1 PHASES

CONSET OF MITOSIS. ITS ACTIVITY INTREASES DURING S AND G1 PHASES

CORRELATED DECREASE AT M PHASE WHEN IT IS HYPERPHOSPHORYLATED A

CORRELATED DECREASEIN PROFIEN LEVEL OCCURS AT M/G1 PHASE,

PROBABLY DUE TO ITS DEGRADATION. SPECIFICALLY PHOSPHORYLATES AND

INACTIVATES CYCLIN B1-COMPLEXED CDC2 REACHING G2

PHASE AND A MINIMUM AS CELLS ENTER M PHASE. PHOSPHORYLATION OF

CC CYCLIN B1-CDC2 OCCURS EXCLUSIVELY ON TYR-15 AND PHOSPHORYLATION OF

CC MONOMERIC CDC2 DOES NOT OCCUR (BY SIMILARITY).
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            ;
0
tyrosine phosphate.

WINTHESIS IS INCREASED DURING S AND G2 PHASES, PRESUMABLY BY AN INCREASE IN TRANSCRIPTION; ACTIVITY IS DECREASED BY PHOSPHORYLATION DURING M PHASE. PROTEIN LEVELS FALL IN M PHASE AS A RESULT OF DECREASED SYNTHESIS COMBINED WITH DEGRADATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                    Length 504;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                   7B05B23268146CDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        053802;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Weel-like protein kinase (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                646 AA
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                    Score 7; I
                                                                                                                                                                                                                      EMBL, AL035569; CAB37577.1; -.
InterPro; IRR003789; DUF186.
InterPro; IPR00173; Gln_amidotransf_B.
Pfam; PF02637; DUF186; 1.
Pfam; PF01162; GatB; 1.
Pfam; PF0343; GatB, 1.
PR0517E; PS01234; GATB, 1.
                                                                                                                                                                                                                                                                                                                                          3.6%; Scor
100.0%; Pre
                                                                                                                                                                                                                                                                                                                   504 AA; 54485 MW;
                                                                                                                                                                                                                                                                                                        Protein biosynthesis; Ligase.
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                  DPVMGLE 84
                                                                                                                                                                                                                                                                                                                                                                                                                      18 DPVMGLE 24
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEE1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                        ENTRY INTO MITOSIS, ALTHOUGH N-TERMINAL PHOSPHORYLATION MIGHT ALSO REGULARF THE PROTEIN STABILITY VIA PROTECTION FROM PROTEOLYSIS OR MIGHT REGULATE THE SUBCELLULAR LOCATION (BY SIMILARITY)
SUBUNIT: BINDS TO 14-3-3 PROTEIN ZETA.
ACTIVITY SEEMS TO BE NEGATIVELY REGULATED BY PHOSPHORYLATION UPON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=S28BC / AB972;
Dietrich E.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
Adviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY CDC2) (POTENTIAL). PHOSPHORYLATION (BY CDC2) (POTENTIAL). 740120F51C811DAF CRC64;
                                                                                                                              -:- SUBCELLULAR LOCATION: Nuclear (By similarity).
-:- PTM: PHOSPHORYLARED DUBING M AND G1 PHASES. ALSO
--- ATTOPHOSPHORYLARED (By similarity).
-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-CCT-1993 (Rel. 27, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 195.4 kDa protein in RPS26B-GLC7 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Комр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS00107; PROTEIN KINASE_ATP: 1.
PROSITE: PS00107; PROTEIN KINASE_ATP: 1.
PROSITE: PS50011; PROFIEIN KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN KINASE_ST: 1.
Mitosis: Transferase; Tyrosine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., F
Wel Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLY.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1753 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.6%; Score 7; DB 1
100.0%; Pred. No. 18;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY - ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D31838; BAA06624.1; -.
EMBL; D31838; BAA06624.1; -.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation; Nuclear protein.
DOMAIN 34 42 POLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
568
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425
123
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                                                                                                                                                                                                                                    WEEL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646 AA;
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298
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P32634;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-!- FUNCTION: MAY PLAY A ROLE IN CARRYING AND ORIENTING CARBOHYDRATE, AS WELL AS HAVING A MORE SPECIFIC ROLE.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD52 entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd52.htm".
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Epididymis;
MEDLINE-93119668; PubMed-8418821;
Kirchhoff C., Krull N., Pera I., Ivell R.;
Kanchoff C., Krull N., Pera I., Ivell R.;
A major mRNA of the human epididymal principal cells, HE5, encodes the leucocyte differentiation CDW52 antigen peptide backbone.";
Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xia M.-Q., Tone M., Packman L., Hale G., Waldmann H.; "Characterization of the CAMPATH-1 (CDw52) antigen: biochemical analysis and cDNA cloning reveal an unusually small peptide
                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CAMPATH-1 antigen precursor (CD52 antigen) (CDW52) (Cambridge pathology 1 antigen) (Epididymal secretory protein E5).
                                                                                                                                                                                                                                                                                                                                     Length 1753;
                                                                                                                                                                                                                                                                                             E4252998C6C2508B CRC64;
                                                                                                                                                                                                                                                                                                                                   3.6%; Score 7; DB 1;
100.0%; Pred. No. 42;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 25-35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Spleen;
MEDLINE=91285018; PubMed=1711975;
                                                                                                                                                                                                                                                                                 l protein.
1753 AA; 195382 MW;
                                                                                                                                                                                                               EMBL; U18916; AAC03230.1; -.
                                                                                                                                                                                                                           PIR; $30855, $30855.
SGD; $5000934; PMD1.
InterPro; IPR001799; Kelch.
Pfam; PF01344; Kelch; 2.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         186 PLEPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
CD52_HUMAN
ID CD52_HUMAN
AC P31358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              backbone."
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92207922; PubMed=1554697; Schluchter WM., Bryant D.A.; Schluchter WM., Bryant D.A.; Molecular characterization of ferredoxin-NADP+ oxidoreductase in cyanobacteria: cloning and sequence of the petH gene of Synechococus sp. PCC 7002 and studies on the gene product."; Biochemistry 31:3092-3102(1992). -i- SIMILARITY: CONTAINS I RESPONSE REGULATORY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                     Antigen; Signal; Glycoprotein; GPI-anchor; Membrane; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
HAPOTORIC (Rel. 41, Last annotation update)
Hypothetical protein in petH 3'region (Fragment).
Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
Bacteria: Cyanobacteria: Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                               REMOVED IN MATURE FORM (POTENTIAL).
GPI-ANCHOR (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_005130.
4AE2A056682BEEA6 CRC64;
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DOMAIN 20 >63 RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                        CAMPATH-1 ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AA
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100.0%; Pred. No. 25;
rative 0; Mismatches
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Pred. No.
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                                                                                                                                                        EMBL; X62466; CAA44323.1; -. EMBL; X67699; CAA47929.1; -. EMBL; A23013; CAA01644.1; -. PIR; S18766; S18766. MIM; 114280; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6614 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Best Local Similarity
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CARBOHYD
CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                               SIGNAL
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168 GLVEAA 173
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A COLE S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
A Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
A Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
A Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
A Holroyd S., Hornsby T., Jagels K., Lacrolx C., Maclean J., Moule S.,
A Murphy L., Oliver K., Guall M.A., Rajandream M.A., Ruther ford K.M.,
A Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
A Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
A Barrell B.G.;
Wature 409:1007-1011/2001).
C. I- FUNCTION: THIS IS ONE OF THE THREE CHAINS OF THE NONENZYMATIC
COMPONENT (FF(0) SUBDUIT) OF THE ATPASE COMPLEX.
C. I- SUBUNIT: R-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) HAS FIVE
SUBUNIT: S. ALFA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
HAS THREE MAIN SUBUNITS: A, B AND C.
C. I- MISCELLANEOUS: DICYCLOHEXYLCARBODIMIDE (DCDD) INHIBITS ATPASE.
C. I- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DICYCLOHEXYLCARBODIIMIDE (BY SIMILARITY).
E5456207EE9E0C13 CRC64;
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrogen ion transport; CF(0); Transmembrane; Lipid-binding;
                                                                                                                                                                                                                                                                                                           ol-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ATP synthase C chain (EC 3.6.3.14) (Lipid-binding protein)
(Dicyclohexylcarbodilmide-binding protein).
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith D.R., Robison K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
;
   Mismatches
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MEDLINE-21128732; PubMed-11234002;
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InterPro: IPR000454; ATPase_C_cub.
Pfan: PF00137; ATP-synt_C; I.
PROSITE; PS00605; ATPASE_C; I.
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   Conservative
                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                      ATPL_MYCLE STA
P45828;
01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1769
                                                                80 VMGLEE 85
                                                                                                         35 VMGLEE 40
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   Matches
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Gaps
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   Length 81;
3.0%; Score 6; DB 1;
100.0%; Pred. No. 33;
tive 0; Mismatches
                                6; Conservative
    Query Match
Best Local Similarity
Matches 6; Conserv
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63 |||||| 58 GLVEAA Search completed: October 4, 2002, 10:20:49 Job time: 232 sec

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	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	11 19 20 20	r r r r	
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Post-processing:	Post-processing: Listing first 45 summaries	44	9	3.0
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Q17620 caenorhabdi Q91211 streptomyce Q91xx6 streptomyce Q91x5 oryza sativ Q94192 homo sapien Q9132 homo sapien Q95031 homo sapien Q95031 homo sapien Q95031 homo sapien Q9743 drosophila Q9746 mus musculu Q9743 drosophila Q94045 thermoanaer Q96045 thermoanaer Q96045 thermoanaer Q9603 homo sapien Q9603 homo sapien Q96045 tatus norv Q9604 tatus no

0217620 099LZL1 099LZL1 094L1S5 094L1S5 096U192 095L10 092L10 092L10 099LC3 099C49 099C49 099C49 090C49 096C93 096

4 11 5

13

10

4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:* sp_unclassified:* sp_rodent:*
sp_virus:*
sp_vertebrate:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_plant:*

. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description	Q97hw9 clostridium	Q96ym2 sulfolobus	Q9hwu2 pseudomonas	Q93j78 streptomyce	Q9h611 homo sapien	Q9s0n6 streptomyce	Q9pus0 salvelinus	, Q9gpq4 trypanosoma	Q9sad4 arabidopsis	Q12953 homo sapien	Q9djr1 citrus tris	Q9fr11 lycopersico	Q52181 synechocyst	Q92rw6 rhizobium m	Q97ce9 thermoplasm	Q9ksz8 vibrio chol
SUMMARIES	ID	Q97HW9	Q96YM2	Q9HWU2	093J78	09н611	9N0S60	09PUS0	Q9GPQ4	Q9SAD4	012953	Q9DJR1	Q9FR11	052181	Q92RW6	Q97CE9	Q9KSZ8
	DB	16	17	16	7	4	7	13	Z	10	4	12	10	7	16	17	16
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de	Query	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6
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1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:*

SPTREMBL_19:*

Database :

Fri Oct

us-09-299-139a-1.rspt

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-JCM 10545 / 7;

VA BANG-1272479;

WA Warabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

WA Wagai Y., Mishijina K., Otsuka R., Nakazawa H., Takahiya M., Kato Y.,

A Nagai Y., Nishijina K., Otsuka R., Nakazawa H., Takahiya M., Kato Y.,

A Nagai Y., Nishijina K., Otsuka R., Nakazawa H., Takahiya M., Kato Y.,

A Noshizawa T., Fanaka T., Kudoh Y., Yamazaki J., Kushida N., Oquchi A.,

A Okika Y., Yamagishi M., Nishimura M., Yamagishi A.,

A Shima T., Kikuchi H.;

A Crenarchaeon, Sulfolobus tokodaii strain?..;

DNA Res. B.123-140(2001)

REBL; AP000989; BAB67255.1;

RHD; AP000989; BAB67255.1;

SEQUENCE 150 AA: 17433 MW; 5262C811B145D43B CRC64;
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Feizer J., Salar M.H., Hancock R.E.W., Lory S., Olson M.V.;
Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                       Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 150; . 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 AA; 19718 MW; B76DED0410BD4308 CRC64;
                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE HISTIDINE TRIAD NUCLECTIDE-BINDING PROTEIN
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Last annotation update)
                 150 AA.
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                 PRT;
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
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                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 406:959-964(2000)
                                                                                                                                Sulfolobus tokodaii.
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121 QEKEYYE 127
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                 096YM2
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Q96YM2
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                                  δ
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL596030; CAC44282.1;
Hypothetical protein.
SEQUENCE 204 AA; 21680 MW; DC2C849468F88AA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tashiro H., Ota T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6%; Score 7; DB 2; Length 204; 100.0%; Pred. No. 34; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

TISSUB-SMALL INTESTINE;
Watanaboe K., Kumagai A., Itakura S., Yamazaki M., Tashiro
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
SEQUENCE 266 AA; 28907 MW; 0A291FB7E1339D56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     O'Neil S., Harris D.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09H611;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ22692 FIS, CLONE HSI11184.
                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 21.7 KDA PROTEIN.
                                                                                                                                           204 AA.
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                                                                                                                                           PRT;
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MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                  SCBAC17F8.10C.
Streptomyces coelicolor.
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Best Local Similarity
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168 GLVEAAP 174
                                      142 GLVEAAP 148
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1902;
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Gaps

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Length 189;

3.6%; Score 7; DB 16;

Pred. No. 32; Mismatches

0;

Conservative

100.08;

Query Match Best Local Similarity Matches 7; Conserv

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Gaps

us-09-299-139a-1.rspt

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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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Eukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Lenz C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pelle R.;
"Molecular cloning and characterization of Trypanosoma (Duttonella)
vivax inosine-adenosine-guanosine preferring (IAG-) nucleoside
                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                       Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydrolase homolog.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF311701; AAG38561.2;
InterPro; IPR001910; IUNH.
Pfam; PF01156; IU_nuc_hydro; 1.
Propom; PD007736; IUNH; 1.
                                                                                                                                                            302 AA; 34037 MW; E44C73477F05C3DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 AA; 36330 MW; 034F9833FF6C2825 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               09GPQ4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1AG-NUCLEOSIDE HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F3F19.1 PROTEIN.
                                                                                                                                                                                                                     3.6%; Score 7; DB 13;
100:0%; Pred. No. 47;
ative 0; Mismatches
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100.0%; Pred. No. 50;
tive 0; Mismatches
            Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                          Best_Local Similarity 100. Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5699;
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                                                                                                                                                                                                                                                                                                     34 RCPPGTY 40
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38 RCPPGTY 44
                                                                                                                                                              SEQUENCE
                                                                                                                                           Receptor.
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Q9SAD4;
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MEDLINE-99380548; PubMed=10449723;

MEDLINE-99380548; PubMed=10449723;

MEDLINE-99380548; PubMed=1049723;

Talked H., Monomiya T., Usami M., Ohta T., Omura S.;

Talked H., Monomiya T., Usami M., Ohta T., Omura S.;

Tanthelmintic macrolide avermectin in Streptomyces avermitilis.";

Tanthelmintic macrolide avermectin in Streptomyces avermitilis.";

The Acad. Sci. Us.A., 96:9509-9514(1999).

REMBL; AB032524; BAA846621, -..

REMBL; AB032524; BAA846621, -..

RIGERPO; IPR000051; SAM_bind.

InterPro; IPR0000
                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces avermitilis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Salvelinus fontinalis (Brook trout) (Brook char).
Salvelinus fontinalis (Brook trout) (Brook char).
Brararyota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
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                                      Length 266;
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                                                                              Indels
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Last sequence update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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100.0%; Pred. No. 45;
iive 0; Mismatches
                               3.6%; Score 7; DB 4;
100.0%; Pred. No. 42;
Live 0; Mismatches
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EMBL; AF156738; AAD56428.1; -.
HSSP; O14763; 1D4V.
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                                                                         7; Conservative
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Matches 7; Conservative
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                                 Query Match
Best Local Similarity
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                                                                                                                                                          104 LLSDCPP 110
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Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                   SEQUENCE FROM N.A
                                          NCBI_TaxID=12162;
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| 128 YEPOHRI 134
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                       osterovirus.
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"The complete sequence of a human hippocampus gene (HHCMA56) shows
homology to developmental genes from Arabidopsis and Brassica napus.";
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.

EMBL: U13395; AAA21465.1;
SEQUENCE 370 AA, 41521 MW; B2FIC523F3ABAEFF CRC64;
Liu S., Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A., Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R., Federspiel N., Theologis A.; "Arabidopsis thaliana chromosome 1 BAC F3F19 sequence."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; AC007357; AAD31052.1; -.
HSSP; 080337; 2GCC.
InterPro; IRRO0147; AP2-domain.
Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELENNT.
ProDom: PD0010423; AP2-domain; 1.
SMART; SM00380; AP2, 1.
SEQUENCE 328 AA; 36319 MW; 66320534B5FCAE6B CRC64;
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100.0%; Pred. No. 50;
tive 0; Mismatches
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100.0%; Pred. No. 56;
tive 0; Mismatches
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Q12953;
Q1-007-1996 (TrEMBLrel. 01, Cr
Q1-NOV-1996 (TrEMBLrel. 01, La
Q1-DEC-2001 (TrEMBLrel. 19, La
OXIDOREDUCTASE.
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(TrEMBLrel. 16, I
(TrEMBLrel. 17, I
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Theologis A.:
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Q9DJR1
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
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Loe H.S., Kim I.J., Chung W.I.;
Submitted (DEC.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF209924; AAG43499.1;
InterPro; IPR001017; Bl_dh.
Pfam; PF00676; Ell_dehydrog; 1.
SEQUENCE 391 AA; 43373 MW; 4ECDBF97E9DD7F46 CRC64;
                                                                                                                                                                                                                                                                                                                                           3.6%; Score 7; DB 12; Length 371; 100.0%; Pred. No. 56; tive 0; Mismatches 0; Indels
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. 59;
STRAIN=PBD5;
CONDOT R.K., Hailstones D.L., Barkley P., Zhou C.;
CONTOT R.K., Hailstones D.L., Barkley P., Zhou C.;
"Characterisation of Australian strains of CTV.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, A1399541; CAC19973.1;
InterPro; IPR000606; Viral_helicasel.
Pfam; PF01443; Viral_helicasel; 1.
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371 AA; 41728 MW; 0B6861589E74684A CRC64;
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Plasmid pCB2.4.
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCB1_TaxID-1148;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PYRUVATE DEHYDROGENASE (FRAGMENT).
Lycopersicon esculentum (Tomato).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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100.0%; Pred. No. 59;
iive 0; Mismatches
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K. Complete proteonome
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                                                                  "The complete DNA sequence and replication analysis of the plasmid pCB2.4 from the cyanobacterium Synechocystis PCC 6803."; Plasmid 31:131-137(1994).
EMBL: L25424; AAAA97418.1; -.
INTERFIC: IPRO3015; HHL.Myc.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE FAD-DEPENDENT OXIDOREDUCTASE PROTEIN.
SMC00779.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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100.0%; Pred. No. 61;
lve 0; Mismatches 0; Indels
                                                                                                                                                                                                                    Length 392;
                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                        392 AA; 42976 MW; 2COFE7A1A8FECB8D CRC64;
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(TrEMBLrel. 18, Last sequence update)
                                                                                                                                                                                                                3.6%; Score 7; DB 2;
100.0%; Pred. No. 59;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              412 AA
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                         STRAIN=PCC 6803;
MEDLINE=94302133; PubMed=8029321;
Yang X., McFadden B.A.,
"The complete DNA sequence and reports." If from the cyanobacterium Sy
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ative 0;
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Best Local Similarity 100.0
Matches 7; Conservative
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Best Local Similarity
'-hes 7; Conserva
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238 EAELKDE 244
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26 PGTEAEL 32
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01-OCT-2001 (
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Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
"Archaeal adaptation to higher temperatures revealed by genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                        Thermoplasma volcanium.
Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 AA; 46443 MW; 40D0C6FBIC84D286 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                sequence of Thermoplasma volcanium,";
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000)
EMBL; AP000991; BAB59294.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.6%; Score 7; DB 17;
100.0%; Pred. No. 64;
ative 0; Mismatches
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InterPro; IPR002293; AA_rel_permease_1.
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Job time: 235 sec
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STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed-11121031;
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Best Local Similarity 10v...
7; Conservative
                  TVG0161955 PROTEIN.
TVG0161955.
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Search time 30.1 Seconds (without alignments) 726.961 Million cell updates/sec
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1 SQPQAVPPYASENQTCRDQE......QSDTTCKNPLEPLPPEMSGT 197
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 version 4.5 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                   747574 seqs, 111073796 residues
                                                                                                  4, 2002, 10:10:57;
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Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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Perfect score:
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/Aa1985.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/Aa1986.DAT:*/SIDS1/gcgdata/hold-geneseqy-embl/Aa1987.DAT:*/SIDS1/gcgdata/hold-geneseqy-embl/Aa1989.DAT:*/SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/Aa1989.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/Aa1989.DAT:* /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1994.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1995.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1996.DAT:* .DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:* /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2000.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2001.DAT:* . DAT: * /SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1991.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990 /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1983. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997 /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980. /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981. /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1982.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Extracellular doma	Human lymphotoxin	Human tumour necro	TNF-R extracellula	Human INF-R extrac	Sequence of a reco	p75 Tumour Necrosi	Primate protein se	Tnfr2 protein. Un	Human soluble tumo	Tumour necrosis fa
SUMMARIES	ΩI	AAW23220	AAY31326	AAB36700	AAW94642	AAB69194	AAR51003	AAR72504	AAY77463	AAB66981	AAW59665	AAW52270
	DB	18	20	22	20	22	15	16	21	22	19	19
	% Query Match Length DB	197	197	415	77	77	518	461	225	227	235	235
	% Query Match	100.0	100.0	0.89	40.2	40.2	27.8	27.3	26.9	26.9	26.9	26.9
	Score	1133	1133	771	456	456	315	309	305	305	305	305
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Tumour necrosis		Z		se 2	40kD TNF inhibitor	F-R	Fibroblast derived	tumour	A human tumour	receptor	TNF receptor	tumour necro	40 kDa	protein	STNFR(075):FC	TNFR:Fc fusion	id se	A K108R/K120R muta	BamTP delta53	Pig costimulatory	Rodent protein seg	e 2	(bgd)	TNFR: Fc fusion	deduced	Tumour necrosis	Peptide fragment	Protease-resistant	Protease-resistant	acid sequenc	Ξ	Ξ	FLINT.
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AAW892	AAY54	AAY54	AAB37	AAY947	AAR1100	AAR111	AAR4205	AAB37	AAB18	AAB0134	AAB3533	AAB36698	AAB37686	AAR2401	AAB70001	AAB5008	AAY54	AAY54	AAR7742	AAY9532	AAY7746	AAY9472	AAB5008	AAB5008	AAR1114	AAY9471	AAB0001	AAB1970	AAB1970	AAB6804	AAY4218	AAB1971	AAY965
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ALIGNMENTS

RESULT

Human; lymphotoxin beta; receptor; blocking agent; extracellular; ligand binding; domain; treatment; Thl cell; immune response; delayed; hypersensitivity; contact; tuberculin; granulomatous; graft versus host; disease; organ rejection; autoimmune; disorder; multiple sclerosis; insulin dependent diabetes; uveitis; cytokine; sympathetic ophthalmia; psoriasis; Listeria; Toxoplasma; infection; Mycobacterium; abnormal; lymphoid organ; development. Extracellular domain of human lymphotoxin beta receptor. Æ AAW23220 standard; protein; 197 (first entry) Homo sapiens 29-0CT-1997 AAW23220;

WO9703687-A1

06-FEB-1997.

96WO-US12010 19-JUL-1996;

95US-0505606

21-JUL-1995;

(BIOJ) BIOGEN INC.

Benjamin CD, Browning JL, Hochman PS;

WPI; 1997-132373/12.

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                                                                          The present sequence, a human lymphotoxin beta receptor (LT-beta-R) blocking agent, comprises the extracellular ligand binding domain confine human LT-beta-R up to the transmembrane region. It can be used to treat a Thl cell mediated immune response which contributes to a delayed type hypersensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity graft versus host disease, organ rejection or an autoimmune disorder, i.e. multiple sclerosis, insulin dependent diabetes, sympathetic conditions exacerbated by the activities of Th-1 type cytokines, or listeria, Toxoplasma or Mycobacterium infection. Its ability to selectively or partially block the LT-beta-R pathway may be useful in the treatment of abnormal lymphoid organ development associated with misexpression or overexpression of signalling by the LT-beta-R pathway. The present LT-beta-R blocking agent is capable of selectively inhibiting Thl, but not Th2 cell dependent immune effector mechanisms. As Thl cytokines can inhibit Th2 cell dependent responses, the present LT-beta-R blocking agent may also indirectly stimulate certain Th2 cell dependent responses which are normally inhibited by Th1 induced cytokines. Doses of about 1 mg/kg of the present soluble LT-beta-R are expected to be suitable get starting doses for optimising treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ta; LT-beta; LT-beta receptor; follicular dendritic cell; tumour; follicular lymphoma; extracellular domain; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
Compositions comprising lymphotoxin-beta receptor blocking agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 1133; DB 18; Length 197; Best Local Similarity 100.0%; Pred. No. 6.7e-84; Matches 197; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lymphotoxin (LT)beta-receptor extracellular region.
              auto:immune diseases, e.g. sclerosis,
                                                    Example 1; Pages 55-56; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY31326 standard; peptide; 197 AA.
                          insulin-dependent diabetes, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09938525-A1
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The invention provides a method for arresting or reducing, severity of effects of a tumour by administration of a composition which inhibits the interaction between lymphotoxin (LT)-beta and its receptor. An inhibitor of the interaction between LT-beta and its receptor can be administered for altering the survival or maintenance of follicular administered for altering the survival or maintenance of follicular organs of the immune system. The method is useful for treating the architecture of the immune system. The method is useful for treating tumours, specifically follicular lymphomas. It offers an alternative therapy for those with tumours resistant to traditional chemotherapy. The present sequence represents the extracellular region of the human LTbeta-receptor and comprises the ligand binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
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                                                                                                                                                                                                                                                                                          New method of treating follicular lymphomas by inhibiting interaction between lymphotoxin-beta and its receptor
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100.0%; Pred. No. 6.7e-84;
ive 0; Mismatches 0;
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                                                                                                                                                            Tsiagbe V;
                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 25-26; 31pp; English
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98US-0073410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TTCKNPLEPLPPEMSGT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                            Thorbecke J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 197; Conservative
                                                                                                                                                                                                                             WPI; 1999-469242/39.
                                                                                               (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200071150-A1.
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   02-FEB-1998;
30-JAN-1998;
                                                                                                                                                                Browning J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2001
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Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
              TNF-R extracellular Cys-rich domain TNF-R-rp.
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  δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MX BX BX SX
                                                                                                                                                                                                                                                      The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor.

Creceptor 5 (TRNF-5 or TR5). TRID has cytostatic, immunosuppressive, noctropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful in the treatment of tumours, resistance to polynuclocities are useful in the treatment of twoours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and cortain autoimmune disease after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID colypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID colides, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; are useful in the diagnosis, treatment or prevention of: (a) cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHC--ELL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                               as tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding a TRID polypeptide, also referred to as tumm necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>``</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.0%; Score 771; DB 22; Length 415; 70.7%; Pred. No. 2.1e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
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                                                                                                                                                                                                                                  Disclosure; Fig 2; 285pp; English
                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94642 standard; peptide; 77
                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                      18-MAY-2000; 2000WO-US13515.
                                                                 99US-0135164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 70.7
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||| ||| ||| || || || 208 sdticknppep 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 SDTTCKNPLEP 189
                                                                                                                                                 WPI; 2001-041051/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-APR-1999
                                                                  20-MAY-1999;
            30-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                       Wei Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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The present invention describes peptides and peptide analogues which correspond in primary sequence to a binding loop of a tumour necrosis factor receptor (TNR-R) superfamily member. The compounds are especially designed from a binding loop of TNR-R p55. They are capable of inhibiting TNR binding to its cellular receptors and may be used to inhibit the biological activities of TNR-They may be used in treating TNR-associated conditions such as acute and chronic inflammatory responses, septic shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic reactions, immune complex disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplantation rejection and malaria. Administration is, e.g. oral, transdermal, transmucosal, pulmonary, subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present sequence represents an extracellular Cys-itch domain of TNF-R from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 VCATCAENSYNEHWNYLTICOLCRPCDPVMGLEEIAPCTSKRKTOCRCOPGMFCAAWALE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New compounds designed from a binding loop of a tumour necrosis factor receptor - are capable of inhibiting the biological activities of tumour necrosis factor, e.g., in treating inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor receptor; TNF-R; autoimmune diseases; inflammation; septic shock; cachexia; graft versus host disease; skin allergic reaction; immune complex disease; malaria; transplantation rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.2%; Score 456; DB 20;
100.0%; Pred. No. 9.2e-30;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Greene MI, Murali R, Takasaki W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB69194 standard; protein; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.01
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                         98WO-US10891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-080781/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 77; Conserv
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                                                                                                                                                                                                                             W09853842-A1
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         29-MAY-1998;
                                                                                                                                                                                                                                                                                             03-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-1997;
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necrosis factor receptor; chimeric antibody molecule;

93WO-US08666 92US-0946236

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immuglobulin
                                                                                                                  14-SEP-1993;
                                                                                                                                       15-SEP-1992;
                                                                    WO9406476-A.
                                                                                            31-MAR-1994
                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                   osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption inhibiting peptide analogues from the present invention have osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory and immunomodulatory activities, and are tumour necrosis factor (TNF) related activation-induced cytokine (TRANCE)/ receptor activator of Wiseases characterised by bone loss such as useful for treating diseases, metastatic bone disease, rheumatoid arthritis or periodontal disease, and modulating dendritic cell maturation; T cell proliferation, and/or CD40 receptor systems. The present sequence represents an extracellular Cysrich domain of a tumour necrosis factor receptor (TNF) superfamily member, which is used in the exemplification of
osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic; antirheumatic; antiarthritic; antiinflammatory; immunomodulatory; tumour necrosis factor-related activation-induced cytokine; TRANCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of a recombinant human (rhu) tumour necrosis factor receptor {\tt TNFR/fc} fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 VCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptides and peptide analogs which are TRANCE/RANK inhibitors
                                 receptor activator of NF-KappaB ligand, RANK, osteoporosis; Paget's disease; metastatic bone disease; rheumatoid arthritis; periodontal disease; modulating dendritic cell maturation; T cell proliferation; CD40 receptor system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for inhibiting
                                                                                                                                                                                                                                                                                                                             for inhibiting osteoclastogenesis and bone resorption
                                                                                                                                                                                                                                                                     Murali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.2%; Score 456; DB 22;.
100.0%; Pred. No. 9.2e-30;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                     Greene MI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR51003 standard; Protein; 518 AA.
                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                     Baron R,
                                                                                                                                                               28-JUL-2000; 2000WO-US20510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 CTHCELLSDCPPGTEAE 128
                                                                                                                                                                                                             (UYPE-) UNIV PENNSYLVANIA. (AOKI/) AOKI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cthcellsdcppgteae 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
'-hag 77; Conserve
                                                                                                                                                                                                                                                                                           WPI; 2001-182866/18.
                                                                                                                                                                                                                      AOKI K.
HORNE W C.
BARON R.
                                                                                                                                                                                                                                                                     Horne WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 AA;
                                                                                                                   WO200108699-A1
                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-0CT-1994
                                                                                                                                                                                      28-JUL-1999;
                                                                                                                                          08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                              BARO/)
                                                                                                                                                                                                                                    HORN/)
                                                                                                                                                                                                                                                                    Aoki K,
                                                                                                                                                                                                                                                                                                                  Jse of
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AAQ45224 is CDNA from clone 1 of library WI-26 VA4 of human fibroblast cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein having a mol. wt. of about 75-80 kba. The cloning of the CDNA for TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1 is contained in expression vector pCNV/NOT-TNFR (ATCC 68088). A recombinant chimeric antibody may be produced having TNFR sequences substituted for the variable domains of either or both of the immunoglobulin molecule heavy and light chains and having unmodified constant region domains. A specific example of a TNFR/FC fusion protein is given in AAQ45225/R51003. The rhu TNFR:FC fusion gene was created by ligating the following fragments into a cloning vector: 1) an 867 bp Asp718-Pvuiz fragment from pCAV/NOT-TNFR (ATCC 68088) contg. the cDNA encoding the truncated TNFR. 2) a 700 bp cettor contg. the FC fragment of human IgG1. 3) An oligo linker; to fuse the truncated TNFR plasmid pIXY498 is a yeast expression contog. The FC fragment of human IgG1. 3) An oligo linker; to fuse the truncated TNFR receptor and the 5' end of human IgG1, and primer AAQ45226, which encodes the 3' end of the truncated TNF receptor and the 5' end of human IgG1, and primer AAQ45220; which encodes the and of the fruncated TNF with the human IgG1, end of them IgG1, and an antisense sequence encoding bps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HWNYLTICOLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 kcrpgfgvarpgtetsdvv----ckpcapgtfsnttsstdicrphqicn---vvaip
                                                                                                                                                                                                                                                          Treating TNF mediated inflammatory diseases with TNF antagonist esp. soluble form of TNF receptor, opt. as fusion protein with human immunoglobulin Fc region, esp. for treating arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
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35.5%; Pred. No. 1.5e-17;
ive 24; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 32-34; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gnasmdavctstsptrsmap 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.8
Best Local Similarity 35.5
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human IgG1
                                                                           Smith CA;
(IMMV ) IMMUNEX CORP.
                                                                                                                                                   WPI; 1994-118172/14.
N-PSDB; AAQ45225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 AA;
                                                                               Jacobs CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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192 gnasmdavctstsptrsmap 211

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RESULT AAR72504

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 lwnwvpeclscgsrcssdqv---etqactreqnrictcrpgwycalskqegcrlcaplr 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A ligand to a member of the tumour necrosis factor (TNF)/nerve growth factor (NGF) receptor family which binds either to the region of the 4th-Cys rich domain of the receptor, or to the region between it and the cell membrane may be used in the production of a pharmaceutical composition for increasing the inhibitory effect of a soluble receptor of the TNF/NGF receptor family. This sequence is the sequence of the p75 TNF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aftpyapepgstcr--lreyydqtaqmccskcspgqhakafctktsdtvcdscedstytq 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor (TNF) receptor ligand - used to increase inhibitory effect of a soluble TNF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                     Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.3%; Score 309; DB 16; Length 461; 35.5%; Pred. No. 4e-17; .ive 24; Mismatches 77; Indels 28
                                                                                                                                                                                                                                                   /note= "Unidentified amino acid."
                                                                                                                                                                                                             258..285
/label= Transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                             Wallach D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p75 Tumour Necrosis Factor Receptor.
                                                                                                                                                                      Location/Qualifiers
27..214
/label= TBPII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 2; 18pp; English.
AAR72504 standard; Protein; 461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           Mett I,
                                                                                                                                                                                                                                                                                                                                                                                   (YEDA ) YEDA RES & DEV CO LTD. (WALL/) WALLACH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                                                  94EP-0116015.
                                                                                                                                                                                                                                                                                                                                                            93IL-0107267.
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 35.5
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Beletsky I, Bigda J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-148673/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ89544.
                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                  11-0CT-1994;
                                                                                                                                                                                                                                                                                                                                                           12-OCT-1993;
                                                  31-OCT-1995
                                                                                                                                                                                                                                                                                                        19-APR-1995
                                                                                                                                                                                                                                                                             EP648783-A.
                                                                                                                      receptor.
                        AAR72504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                    Region
                                                                                                                                                                                                             Domain
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The invention relates to a number of primate and/or rodent proteins, and the genes which encode them. The invention encompasses human dendritic cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis factor) receptor family-related proteins HPTER84, HSLUD37R and RANKL; human CC chemokine HCC5; human deubiquitinating proteins Dubl1 and Dub 12; human Mo-1 and human and murine MD-2 proteins, which exhibit the properties of ligands for proteins comprising a leucine-rich motif (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies against these proteins. The proteins can be used for modulating the physiology or development of a cell. They can be used to mediate uptake of substrates (e.g., prostaglandin-like molecules), to modulate or mediate cellular interactions (e.g., induce or prevent trafficking, proteins which are important in various cellular processes such as the deubiquitination of proteins or call cycle regulation. The products can be used for treating medical conditions such as immune, inflammatory or be used for treating medical conditions and as immune, inflammatory or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune thyroiditis, as well as acute and chronic inflammatory responses in which T cell activation, expension, and/or immunological T cell memory play an important role. Sequences AAY77463-Y77464, AAY77474-Y77475 and AAY77484 represent primate proteins of undefined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function, AAY77462 and AAY77481 are rodent proteins of undefined function, and AAY77482 is an avian protein of undefined function. These sequences are given in the sequence listing but are not referred to in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     allergic disorders, or abnormal cellular proliferation, for example, cancers or degenerative conditions. They can be used to modulate immune responses in disease states e.g., autoimmune disorders, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnston JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated mammalian genes, used to develop products for treating e.g. immune, inflammatory or allergic abnormalities, cancers or
                                                                                                                                                                                                                                                                                                          Imune disorder; inflammation; allergy; immunosuppressant;
antiarthritic; antirheumatoid; antiinflammatory; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gorman DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EE, Mattson JD, Gorman
Murgolo NJ, Greene JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 170-171; 218pp; English.
                                                                                                                                                                                                                             Primate protein sequence, SEQ ID NO:14.
AAY77463 standard; Protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lebecque SJE, Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zlotnik A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lees EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0110938.
98US-0114466.
98US-0093897.
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98US-0136214.
98US-0099999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       degenerative conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hedrick JA, Wang L,
Bazan JF, Mahony D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-171015/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200001817-A2.
                                                                                                                                                 05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-AUG-1998;
18-AUG-1998;
11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                           antithyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1998;
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23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bates EEM,
                                                                            AAY77463;
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WPI; 1998-333039/29.
N-PSDB; AAV41549.
                                                                                                                                                                        Local Similarity
nes 70; Conserv
                                                                                                                                   · 227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9824463-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-1997
                                                                                                                                    Sequence
                                                                                                                                                                  Query Match
                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                      192
                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
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                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                  multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute panoreatitis; Alzhelmer's disease; anorexia; atherosclerosis; pain; coronary condition; myocardial infarction; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; ischaemia; Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57080 AAF57080 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor necrosis factor alpha -
                                                                                                                                    64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                       141
                                                                                                                                                                                        DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                        Gaps
                                                                                                              85
                                                                                          5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                         Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
                                                                                                                                             28;
                                                  Length 225;
                                                                       Indels
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                                                       4e-17;
                                                 DB 21;
                                               26.9%; Score 303; 35.0%; Pred. No. 4e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chang M,
                                                                                                                                                                                                                                                                                           Š
the remainder of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calzone FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 316pp; English.
                                                                                                                                                                                                                                                                                         AAB66981 standard; Protein; 227
                                                                                                                                                                                                                    GTAQSDTTC -- KNPLEPLPP 192
                                                                                                                                                                                                                                       gnasmdavctstsptrsmap 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0350670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-2000; 2000WO-US18667
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lacey DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-103031/11.
                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                    225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200103719-A2
                                                                                                                                                                                                                                                                                                                                                      Infr2 protein.
                                                                                                                                                                                                                                                                                                                                  19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-2001
                                                                       70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boyle WJ,
                                                                                                                                                                                                                                                                                                               AAB66981;
                    Sequence
                                                   Query Match
                                                                                                                                                                                                                                       192
                                                                                                              28
                                                                                                                                                                            120
                                                                       Matches
                                                                                                                                                                                                                                                                              AAB66981
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modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), anomer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, promises and septic shock. The present sequence was used in a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 lwnwvpeclscgsrcssdqv---etqactreqnrictcrpgwycalskgegcrlcaplr 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treatment of acute or chronic inflammatory disease, e.g. leukaemia - by administering tumour necrosis factor binding protein and at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 aftpyapepgstcr--lreyydqtaqmccskcspgqhakvfctktsdtvcdscedstytq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tumour necrosis factor; TNF; TNF receptor type II; inflammatory disease; leukaemia; TNF binding protein; anti-inflammatory drug; methotrexatess.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human soluble tumour necrosis factor receptor type II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.le-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĎΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.9%; Score 305; Dp
35.0%; Pred. No. 4.1e
tive 24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW59665 standard; Protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 GTAQSDTTC - - KNPLEPLPP 192
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96US-0032587.
97US-0036355.
97US-0039315.
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Similarity
                                                                                                                                                                                          235 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 70;
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                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Soluble tumour necrosis factor receptor; sTNFR; TNF-mediated disease; tumour necrosis factor binding protein; autoimmune disease; arthritis; adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy; tumour necrosis factor inhibitor; Alzheimer's disease; TNBP.
                                                                                                                                                                                                                       HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                  DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                     This is the amino acid sequence of the human tumour necrosis factor receptor type II, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.
                                                                                                                                                   Gaps
                                                                                                                                                                                 5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Truncated and soluble forms of tumour necrosis factor receptor - useful for treating diseases involving factor, e.g. arthritis and adult respiratory distress syndrome
                                                                                                                                 Length 235;
                                                                                                                                                   78; Indels
one additional anti-inflammatory drug, e.g. methotrexate
                                                                                                                               26.9%; Score 305; DB 19; 35.0%; Pred. No. 4.2e-17; iive 24; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                              AAW52270 standard; Protein; 235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kieft GL;
                    Disclosure; Fig 2; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor inhibitor.
                                                                                                                                                                                                                                                                                          GTAQSDTTC--KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                              gnasrdavctstsptrsmap 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0039792.
96US-0021443.
96US-0032534.
97US-0037737.
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                                                                                                                                       Local Similarity 35.08 tes 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fisher
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                                                                                                 235 AA;
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09-JUL-1996
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                                                                                                 Sequence
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                                                                                                                                Query Match
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                                                                                                                                        Best Loca
Matches
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This sequence is the human tumour necrosis factor inhibitor. The protein was used to make the truncated soluble tumour necrosis factor receptor (gTNFR) proteins of the invention. The truncated sTNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g. arthritis, adult respiratory distress syndrome, cacheria/Anorexia/Anorexia/Anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexia/anorexi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 305; DB 19;
Pred. No. 4.2e-17;
4; Mismatches 78;
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3; Fig 8; 205pp; English.
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35.0%;
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an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated Al monomers; (2) an isolated nucleic acid encoding Al; (3) an expression vector comprising the nucleic acid encoding Al; (3) an expression vector comprising the nucleic acid expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNF)/OPG chimeras are used to treat TNF and TNFF, mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The fused heterologous sequences to identify potential new receptors with fladds. The present sequence represents the TNF inhibitor 40 kDa
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6
                                                                                                                   present invention describes a chimeric polypeptide (A1), comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p75 tumour necrosis factor receptor; mutant; PEG conjugated protein; polyethylene glycol conjugation; PEG conjugation; protein activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a K108R mutant of soluble p75 TNF receptor.
            New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.9%; Score 305; DB 20; 35.0%; Pred. No. 4.2e-17; ive 24; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
108
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                                                                                 Disclosure; Fig 3; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                           235 AA;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                             protein.
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The present sequence represents a N-terminal fragment of a mutant of the soluble tumour necrosis factor (TNF) receptor, where the wild the soluble tumour necrosis factor (TNF) receptor, where the wild cype to state the soluble tumour necrosis factor (TNF) receptor and ligand. These residues are also potential polyethylene glycol (PEG) conjugation sites. The wild type p75 TNF receptor protein was mutated and conjugated to PEG, using the method of the invention. The specification descries a method for conjugating proteins with PEG to result in PEG-conjugated proteins having little or no reduction in a desired activity. Specifically, one or more amino acid residues that are critical for protein bioactivity and which are capable of reacting with PEG sites are deleted, prior to conjugation of the protein to PEG. The methods provide PEG conjugated proteins that are more homogeneous and present in higher yields. Conjugation does not take place at amino acid residues that are are critical to the proteins bioactivity, thus maintaining the activity of the protein. The methods are used to produce PEG conjugated proteins.
                                                                                                                                                                                   Novel methods for site-specific protein modification by mutagenesis by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 HWNYLTICQICR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 lwnwypeclscgsrcssdqv---etgactregnrictcrpgwycalsrgegcrlcaplr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p75 tumour necrosis factor receptor; mutant; PEG conjugated protein; polyethylene glycol conjugation; PEG conjugation; protein activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.9%; Score 305; DB 21; 35.0%; Pred. No. 4.2e-17; ive 24; Mismatches 78;
                                                                                                                                                                                                     replacing polyethylene glycol reacting sites
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                                                                                                                                                                                                                                          Claim 17; Page 29; 36pp; English.
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                                                    (IMMV ) IMMUNEX CORP.
                                                                                                                               WPI; 2000-160577/14.
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Best Local Similarity
Matches 70; Conserva
                                                                                                                                                N-PSDB; AAZ45759
               22-JUN-1998;
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                                                                                           Pettit DK;
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Homo sapiens
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                                                                                                                                                                                                                                                             tumour necrosis factor (TNE) receptor. The wild type Lys residues at positions 108 and 120 are replaced with Arg (see AAY5441-42). Lys120 and Lys108 make contact between the p75 receptor and ligand. These residues are also potential polyethylene glycol (PEG) conjugation sites. The wild type p75 TNF receptor protein was mutated and conjugated to PEG, using the method of the invention. The specification descries a method for conjugating proteins with PEG to result in PEG-conjugated proteins with PEG to result in PEG-conjugated proteins with PEG to result for cativity. Specifically, one or more amino acid residues that are activity. Specifically, one or more amino acid residues that are critical for protein bioactivity and which are capable of reacting with PEG sites are deleted, prior to conjugation of the protein to PEG. The methods provide PEG conjugation does not take place at amino acid residues that are are critical to the proteins bioactivity, thus maintaining the activity of the protein. The methods are used to produce PEG conjugated proteins. The methods are used to produce PEG conjugated proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                   Novel methods for site-specific protein modification by mutagenesis by replacing polyethylene glycol reacting sites \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 HWNYLTICOLCR----PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin; LL-1; inflammatory disease; degenerative disease; human; lymphotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                     present sequence represents a N-terminal fragment of the soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.9%; Score 305; DB 21; Length 235; 35.0%; Pred. No. 4.2e-17; ive 24; Mismatches 78; Indels 2
                                                                                                                                                                                                                         Claim 16; Page 35-36; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB37685 standard; Protein; 235 AA.
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                                      99WO-US13953
                                                                98US-0102530
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                                                                                         (IMMV ) IMMUNEX CORP.
                                                                                                                                           WPI; 2000-160577/14.
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                                                                                                                                                          N-PSDB; AAZ45762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 40 kDa
                                      18-JUN-1999;
                                                                22-JUN-1998;
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            29-DEC-1999
                                                                                                                     Pettit DK;
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The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 lwnwypeclscgsrcssdqv---etgactregnrictcrpgwycalskqegcrlcaplr 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 kcrpgfgvarpgtetsdvv----ckpcapgtfsnttsstdicrphgicn---vvaip 169
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                                                                                                                                                                                                                                                                                                                                                                                              Brewer MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4, 2002, 10:12:22
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RW, Vannice J, Kohno T;
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89US-0381080.
89US-0450329.
90US-0479661.
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Job time: 85 sec
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                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 AA;
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US6143866-A.
                                                                                                        19-JAN-1995;
                                                                                                                                                               19-JUL-1990;
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                                                       07 - NOV - 2000
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11-DEC-1989
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us-09-299-139a-1_1.rai

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4, 2002, 10:10:57; Search time 13.38 Seconds (without alignments) 359.629 Million cell updates/sec
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1133
1 SQPQAVPPYASENQTCRDQE......QSDTTCKNPLEPLPPEMSGT 197
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-975-448
US-08-795-4478-48
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US-08-795-4468-48
US-08-95-2468-48
US-09-326-394-4
US-08-35-29-2
US-08-650-000-2
US-08-650-000-2
US-08-477-347-3
US-08-477-347-3
US-08-477-347-3
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US-08-650-000-4
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Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Sequence 4, Appli Sequence 5, Appli Sequence 9, Appli

Sequence

Sequence 13, Sequence 5,

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US-09-042-785A-8

Sequence 2, Appli Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl Sequence 10, Appl Sequence 10, Appl Sequence 17, Appl Sequence 17, Appl Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli	•	RECEPTORS AND RAND LIGAND ANTIBODIES AS IE TREATMENT OF IMMUNOLOGICAL30
.2 300 2 US-08-794-796-2 .0 625 3 US-08-996-139-15 .0 625 4 US-09-915-659-15 .5 276 4 US-09-041-886-27 .5 277 4 US-09-042-85A-10 .4 451 3 US-09-996-529-17 .4 451 3 US-09-996-59-1 .4 591 4 US-09-215-649A-2 .5 277 4 US-09-042-85A-10 .6 299 4 US-09-286-529-17 .6 451 3 US-08-996-659-1 .7 591 4 US-09-215-649A-2 .7 591 4 US-08-996-659-6 .8 616 4 US-08-996-659-6 .9 616 4 US-08-996-698-6 .1 616 4 US-08-215-649A-6 .1 616 2 US-08-215-649A-6	ALIGNMENTS	US/08505606 Us/08505606 Christopher D. Christopher D. Paula S. SOLUBLE LYMPHOTOXIN-BETA ANII-LYMPHOTOXIN RECEPTOR THERAPEUTIC AGENTS FOR TH DISBASE 1 S. Haley, Jr. e of the Americas PC-DOS/MS-DOS Release #1.0, Version #1 ATTA: US/08/505,606 L-1995 ATTA: US/08/505,606 L-1995 ATTA: US/08/505,606 L-1995 ATTON: US/08/505,606 L-1955 ATTON: US/08/505
28 285.5 29 283 255 31 283 255 31 283 255 32 277 24 33 277 24 34 277 24 40 277 24 41 277 24 42 277 24 43 277 24 45 277 24 45 277 24 45 277 24 45 277 24 45 277 24 45 277 24		RESULT 1 US-08-505-606-1 Sequence 1, Application US/085056 Patent No. 592531 Patent No. 592531 Patent No. 592531 APPLICANT: BROWNING, Jeffrey APPLICANT: HOCHMAN, Paula S. TITLE OF INVENTION: SOLUBLE L TITLE OF INVENTION: ANTI-LEMPE TITLE OF INVENTION: ANTI-LEMPE TITLE OF INVENTION: ANTI-LEMPE TITLE OF INVENTION: ALBAPY, STREET: 1251 Avenue of the CITY: New York STREET: 1020 CONFESSEE: James F. Haley, STREET: New York STREET: New York COUNTRY: U.S.A. ZIP: New YORK STREET: New YORK STREET: New YORK CONFUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMFUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMFUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMFUTER: BAPTICATION DATA: APPLICATION NUMBER: US/08/5 FILING DATE: 21-JUL-1995 CLASSIFICATION NUMBER: US/08/5 FILING DATE: 26-JAN-1995 ATTORNEY/AGENT INFORMATION: NAME: HALEY, JT., James F. REGIESTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: B1 TELECOMMUNICATION NUMBER: 27,794 REFERENCE/COCKET NUMBER: B1 TELECOMMUNICATION NUMBER: CALLS SEQUENCE CHARACTERISTICS: LENGTH: 197 amino acids TELENGTH:

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Sequence 3, Application US/08866545;
Patent No. 626535
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Takasaki, Wataru
APPLICANT: 
     61 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHC--ELL 118
                                                                                                                             52 VCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE 111
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100.0%; Pred. No. 2.7e-36;
Live 0; Mismatches 0;
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ER: 009113-0004-999
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: COTUZZI, LAUTA A REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: No. 6265535e
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LENGTH: 77 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650-493-5556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 30-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| |||| |||
208 SDTICKNPPEP 218
                                                                                                                                                                                                         SDTTCKNPLEP 189
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                               US-08-866-545-3
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                                                                                                                                                                                                       121 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                1 SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
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  Length 197;
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                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WEI, YING-FEI
APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
ITILE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR (WINGERS OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
100.0%; Score 1133; DB 2;
ilarity 100.0%; Pred. No. 1.2e-99;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%; Score 771; DB 4; 70.7%; Pred. No. 3.6e-65; iive 14; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09006353A Patent No. 6261801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TTCKNPLEPLPPEMSGT 197
                                                                                                                                                                                                                                                                                                                                                                                                                 181 TTCKNPLEPLPPEMSGT 197
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Best Local Similarity
Matches 135; Conserv
                            Similarity
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                                                    Matches 197;
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       Query Match
                               Best Local
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64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQ 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 227;
                                                                                                                                                                                                                                                                                                                             OPERATING STSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 305; DB 4;
Pred. No. 1.6e-21;
4; Mismatches 78
    APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BOYLE, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-795-447A-48; Sequence 48, Application US/08795447A; Patent No. 6284728; GENERAL INFORMATION:
                                                                                                                           ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
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Best Local Similarity 35.0%; Pre
Matches 70; Conservative 24;
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-795-445A-48
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                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc
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CLASSIFICATION:
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                                                                                                                                                                             CITY: The
STATE: Ca
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFONTSSPSARCOPHTRCENOGLVEAAP 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.9%; Score 305; DB 3; Length 22°35.0%; Pred. No. 1.6e-21;
Live 24; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
                                                                                                                                                                    APPLICANT: BOYJE, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/974,022
12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-795-445A-48; Sequence 48, Application US/08795445A; Pattent No. 628448; Extent No. 628448; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Amgen Inc.
STREEF: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                                                                         Sequence 48, Application US/08974022
Patent No. 6015938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 GTAQSDTTC -- KNPLEPLPP 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
'LENGTH: 27 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Boyle, Willaim J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 35.09
Matches 70; Conservative
61 CTHCELLSDCPPGTEAE 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                 US-08-974-022-48
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64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                             Length 227;
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Llarity 35.0%; Pred. No. 1.6e-21;
Conservative 24; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
ITILE OF INVENTION: OSTEOPROTECERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/795,446B
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/08795446B Patent No. 6288032
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Amgen Inc.
1840 Dehavilland Drive
                                                                                NAME: Winter, Robert B.
REFERRNEC/POCKET WUMBER: A
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 GTAQSDTTC -- KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNASRDAVCTSTSPTRSMAP 211
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                                                         ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Winter, Robert B. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 amino acids
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                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-974-186-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CITY: Thousand Oaks
STATE: California
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Best Local Similarity
Matches 70; Conservē
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ZIP: 91320-1789
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US-08-795-446B-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.9%; Score 305; DB 4; Length 227; 35.0%; Pred. No. 1.6e-21; tive 24; Mismatches 78; Indels
                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTLN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
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APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TILLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
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: 1840 Dehavilland Drive
Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-974-186-48
; Sequence 48, Application US/08974186
; Patent No. 6284740
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                   COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: P.
INFORMATION FOR SEO ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                  : 227 amino acids
amino acid
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Best Local Similarity 35.0%
                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 514
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ADDRESSEE: Amgen Inc
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COUNTRY: USA
ZIP: 91320-1789
California
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                                        91362-1789
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235 amino acids
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Matches 70; Conser
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 LENGTH:
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                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                   120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                       5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bendele, Alison M.
APPLICANT: Sennello, Regina M.
APPLICANT: Edwards, Carl K.
TITLE OF INVENTION: COMBINATION THERAPY USING A TWF BINDING
                                                                                                                    26.9%; Score 305; DB 4; Length 227; ilarity 35.0%; Pred. No. 1.6e-21; Conservative 24; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATA:
FILIA DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,587
FILING DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,355
*FILING DATE: 23-JAN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/039,315
FILING DATE: 07-FEB-1997
PRIOR APPLICATION DATA:.
APPLICATION NUMBER: US 60/052,023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/09/326,394
08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-326-394-4; Sequence 4, Application US/09326394; Patent No. 6306820
                                                                                                                                                                                                                                                                                                                                                                                                                               192 GNASRDAVCTSTSPTRSMAP 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Zindrick, Thomas K. REGISTRATION NUMBER: 32,1
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                  single
                                                 ; MOLECULE TYPE: protein US-08-795-446B-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                            Query Match
Best Local Similarity
Matches 70; Conserv
amino acid
                                   linear
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              STRANDEDNESS:
TOPOLOGY: lin
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Patent No. 5605690
GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TNF'Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                    64 LWNWVPECLSCGSRCSSDQV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
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                                                                                                                                                                                                                                               5 AVPPYASE-NOTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                             26.9%; Score 305; DB 4; Length 235; 35.0%; Pred. No. 1.6e-21; live 24; Mismatches 78; Indels
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APPLICATION NUMBER: US/07/946,236
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51 University Street
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ZIE: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
"""TER: IBM PC COMPATIble
""""" PC DOS/MS-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 GNASRDAVCTSTSPTRSMAP 189
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TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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amino acid
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                               Conservative
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                  TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-326-394-4
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STATE: Washington
amino acid
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                                                                                                                                                                                                                86 LWNWVPECLSCGSRCSSDQV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 141
                                                                                                                                                                                                                                                             120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                      142 KCRPGFGVARPGTETSDVV-----CKPCAPGTFSNTTSSTDICRPHQICN----VVAIP 191
                                                                                                            28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDIVCDSCEDSTYTQ 85
                                                                                   5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
26.9%; Score 305; DB 1; Length 461; 35.0%; Pred. No. 3.4e-21;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
                                           24; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31,680
3R: 2501-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Wight, Christopher L. REGISTRATION UNDRER: 31,680
REPERENCE/DOCKET UNDRER: 2501
TELECOMMUNICATION INFORMATION: TELEFONE: (206) 287-0430
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                   175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                          192 GNASMDAVCTSTSPTRSMAP 211
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                                           Conservative
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               Best Local Similarity
Matches 70; Conserv
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STATE: Wash
COUNTRY: U.
ZIP: 98101
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Query Match
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64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
BUSIGLED, Samantha J
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 31
CORRESPONDENCES: 31
CORRESPONDENCES: 31
CORRESPONDENCES: 31
STREET: 28 State Street
                                                                                                                                                                                                            5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                      28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQ 85
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                                                                                                                        Length 461;
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 305; DB 4;
Pred. No. 3.4e-21;
                                                                                                                        26.9%; Score 305; DB 2;
35.0%; Pred. No. 3.4e-21;
tive 24; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/042,785A FILING DATE: 17-MAR-1998 PRIOR APPLICATION DATA: BAPLICATION NUMBER: US 08/938,896 FILING DATE: 26-SEP-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 GTAQSDTTC--KNPLEPLPP 192
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SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.9%;
35.0%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 461 amino acids amino acid
                                                                                                                        Query Match
Best Local Similarity 35.0%
Matches 70; Conservative
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                                   ; MOLECULE TYPE: protein US-08-650-000-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 28 State Stre
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
amino acid
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Best Local Similarity
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; FRAGMENT TYPE:
US-09-042-785A-7
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                    FOPOLOGY:
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86 LWNWYPECLSCGSRCSSDQV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 141
                                                                           64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                      64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
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                         5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-006-353A-4
; Sequence 4, Application US/09006353A
; Patent No. 6261801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                                                                                                                                                                 192 GNASMDAVCTSTSPTRSMAP 211
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 461 amino acids TYPE: amino acid
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Best Local Similarity 35.0%
Matches 70; Conservative
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COMPUTER READABLE FORM:
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STATE: M
COUNTRY:
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                                                                                                              HWNYLTICQLCR----PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                   120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
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                                                          28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQ 85
                                    5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
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   Indels
 78;
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 24; Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, 1gor
APPLICANT: BELETSKY, 1gor
TITLE OF INVENTION: THE LIGANDS
NOMBER OF SEQUENCES: 17
COMBER OF SEQUENCES: 17
COMBESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 Seventh Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/115,685
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08477347
Patent No. 6232446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amir.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                               175 GTAQSDTTC--KNPLEPLPP 192
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APPLICATION NUMBER: IL 10
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Townsend, G. Kevin REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WALLACH, David
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amino acid
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 Conservative
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Best Local Similarity
Matches 70; Conserv
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APPLICANT: WALLAC!
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STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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70;
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120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                             5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
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Best Local Similarity 35.0%; Pred. No. 3.4e-21;
Matches 70; Conservative 24; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: THE INHIBITORS NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROGRAPHICATION 1439
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
PRIDING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18 B9
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                       RESULT 15
US-08-476-862-2
Sequence 2, Application US/08476862
Patent No. 6262239
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, IGOT
APPLICANT: METT, IGOT
APPLICANT: ENGELMANN, HARTMUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                     175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                             192 GNASRDAVCTSTSPTRSMAP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 461 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-476-862-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
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Oy 64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCOPGMFCAAWALE-CTHCELLS 119

bb 86 LWNWVPECLSGSRCSSDQV---ETQACTREGNRICTCRPGWYCALSKGEGCRLCAPLR 141

Cy 120 DCPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCOPHTRCENOGLVBAP 174

bb 142 KCRPGFGVARPGTETSDVV-----CKPCAPGTFSNTTSSTDICRPHQICN----VVAIP 191

Oy 175 GTAQSDTTC--KNPLEPLPP 192

bb 192 GNASMDAVCTSTRSMAP 211

Search completed: October 4, 2002, 10:11:19
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- protein search, using sw model OM protein

Run on:

October 4, 2002, 10:10:57; Search time 19.61 Seconds (without alignments) 965.303 Million cell updates/sec

Title:

US-09-299-139A-1 1133 1 SQPQAVPPYASENQTCRDQE......QSDTTCKNPLEPLPPEMSGT 197 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Aaximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	tion	tumor necrosis fac	necrosis fa	necrosis	murine tum	B-cell activation	B cell-associated	death receptor-6 -	OX40 antigen precu	gene ox40 protein	tumor necrosis fac	hypothetical prote	qene G4R protein -	G2R protein - vari		OX40 homolog - hum	tumor necrosis fac	CD30 antigen precu	lymphocyte activat	T2 protein - rabbi	FAS soluble protei	tumor necrosis fac	T2 protein - myxom	apoptosis-mediatin	T-cell antiqen 4-1	nerve growth facto	membrane qlycoprot	nerve growth facto	apoptosis-mediatin	nerve growth facto
SUMMARIES	£ .	418	A35356	B38634	I48854	A60771	A46476	JC7705	S12783	148700	GQHUT1	T28623	D36858	D72175	JC4302	137552	GQMST1	A42086	138426	B43692	137383	GQRTT1	GQVZML	A40036	B32393	A26431	JC5486	JN000E	A46484	GOHUN
	DB	~	П	7	7	7	7	7	7	~	Н	7	7	7	7	7	Н	~	7	7	7	Н	_	7	N	Т	7	Н	7	-
	Query Match Length	4	461	474	459	277	305	651	271	272	455	348	349	349	461	277	454	595	255	325	314	461	326	335	256	425	493	416	327	427
о¥	Query Match	0	26.9	26.0	2	24.5	Н	20.0	19.6	18.9	18.6	18.5	18.5	18.3	18.2	17.7	17.7	17	П	П	_	П	Н	-	_	15.1	14.7	•	14.3	13.1
	Score	1133	305	295	290	278	243.5	226.5	222.5	214.5	210.5	210	210	207	206	201	201	196	195.5	189	187.5	184.5	183.5	181	179.5	171.5	9	9	162	148.5
	Result No.		7	ო	4	5	9	7	ω	σ,	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	53

tumor necrosis factor receptor 2 precursor [validated] - human
NyAlternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Decies: 10-8ep-1999 #sequence_revision 10-8ep-1999 #text_change 08-Dec-2000
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990

181 TTCKNPLEPLPPEMSGT 197

Dp ŏλ g

Fas antigen precur	CD27 antigen precu	hypothetical prote	hypothetical prote	laminin alpha-1 ch	furin (EC 3.4.21.7	cysteine rich prot	laminin alpha 5 ch	hypothetical prote	subtilisin-like pr	subtilisin-like pr	heparan sulfate pr	furin (EC 3.4.21.7	Delta-4 protein -	DELTA-like 1 - mou	subtilisin-like pr
						-									
JC2395	A46517	T26972	T27283	MMMSA	T43251	T42017	T10053	T29764	G02428	JC6148	S18252	A43434	JC7569	148324	A48225
7	-	~	7	Н	7	7	7	7	7	7	7	7	7	7	Н
324	260	1111	1620	3084	1299	1274	3635	2180	899	915	3707	1680	686	722	915
12.8	11.7	11.7	11.4	11.4	11.3	11.3	11.1	11.1	11.0	11.0	11.0	10.9	10.9	10.9	10.8
145.5	133	132.5	129.5	129	128.5	128	126	125.5	124.5	124.5	124.5	124	123.5	123	122.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 154182	JLT 1
tumc	tumor necrosis factor receptor 2-related protein - human
S'S	pecies: Homo sapiens (man)
C; D	C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
2 6	COCCESSION 104104 W. Coccedent T. T. War Box Documber H. Moureson D. Coccession H. Moureson D.
N; D;	Nobello, m.; Challanet, m.; Cassillan, C.C.; Van Gen Bergne, n.; Marynen, F. Coopello, 16, 0114-010 1003
A:T	July 10, 214, 410, 1733. July 21, 214, 410, 1733.
A; Re	I54182; MUID:93252381
A; A	A; Accession: I54182
A;S1	A;Status: preliminary; translated from GB/EMBL/DDBJ
A; W	A Molecule type: mkNA
X . 4	A):MESIQUES: 1-43-3 CKES. A.Crose-references: GB:164270: NID:0330761: DIDN:ABA36757 1: DID:0339762
; č	Constitution of the control of the c
A; Ge	A; Gene: GDB: LTBR
A; C1	ross-references: GDB:1230195; OMIM:600979
A; W	A;Map position: 12p13.3-12p13.1
ດ; ຣາ	C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
ā	100.08;
ž Ř	Similarity 100.0%; Pred. No. 1.4e-78; 7: Conservative 0: Mismatches 0:
Ĕ	of the second se
. 0y	1 SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
qa	28 SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 87
ζŎ	61 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 120
q	88 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 147
Qy	121 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
QQ	

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Habbas factor receptor type 2 precursor - mouse
C:Species: Mas musculus (house mouse)
C:Date: 30-Unn-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: B38634, A40224; S54016
C:Accession: B38634, A40224; S54016
C:Accession: B38634, A40224; S54016
C:Accession: B38634, A40224; S54016
C:Accession: B38634, MUD:91187885
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A:Reference number: A38634; MUD:91187885
A:Accession: B38634
A:Molecule type: MRNA
A:Residues: 1-474 <LEM
A:Accession: B38634
A:Accession: B38634
A:Accession: B38634
A:Accession: B38634
A:Accession: B38634
A:Accession: A40254; MUD:9124818
A:Accession: A40254
A:Molecule type: MRNA
A:Residues: 1-474 <COO
A:Accession: A40254
A:Molecule type: MRNA
A:Residues: 1-2 <ACC
A:Accession: A40254
A:Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 HWNYLTICOLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                           F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <LNT>
F;171,193/Ainding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 LWNWVPECLSCGSRCSSDQV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 PYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWN
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                                                                                                                                                                                                                                                                                                                                           26.9%; Score 305; DB 1;
35.0%; Pred. No. 5.4e-16;
iive 24; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;166-203/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 GNASMDAVCTSTSPTRSMAP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                       70; Conservative
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Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
B38634
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A; Status: preliminary
A; Molecule type: mRNA; protein
A; Molecule type: mRNA; protein
A; Molecule type: mRNA; protein
A; Residues: 23-461 CDEMA
A; Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A; Cross-reference extracted from NCB1 Deackbone (NCBIN:63368, NCBIP:63371)
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A; Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra A; Accession: A36007; MUID:90349572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Cloning, sequencing and partial functional characterization of the 5' region of A;Reference number: I38094; MUID:95121934
A;Accession: I38094
                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur A;Reference number: A36475; MUID:91045991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule, type: mRNA

A; Residues: 1-15; Kr, 197-461 (KOH)

A; Residues: 1-15; Kr, 197-461 (KOH)

A; Cross-references: GB:M55994; GB:M35549; NID:g339757; PIDN:AAA36755.1; PID:g339758

R; Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.

Cytokine 2, 231-237, 1990

A; Title: Two human TWF receptors have similar extracellular, but distinct intracellular,

A; Reference number: A48416; MUID:91370690
A;TILLE: A receptor for tumor necrosis factor defines an unusual family of cellular and A;Reference number: A35356; MUID:90260639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nec
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A Molecule type: protein
B Molecule type: protein
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A; Residues: 116-140, 'P',142-195,'R',197-362,'T',364-461 <HEL>
A; Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
A; Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990
A; Title: Purification and partial amino acid sequence analysis of two distinct tumor A; Ascerence number: A23666; MUID:91056048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: the list of introns is incomplete
C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C; Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <AMAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;120-162/Domain: NGF receptor repeat homology <NG3>
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A;Molecule type: DNA
A;Residues: 1-37 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:TNFR2
A;Cross-references: GDB:125914; OMIM:191191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O.; Wallach,
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A;Molecule type: protein
A;Residues: 27-31 <ENG>
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Gene 150, 381-386, 1994
                                                                                                                                                                                                                                                                                               A; Residues: 1-461 <SMI>
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                                                                                                                                                                                             Status: preliminary
                                                                                                                                                                                                                                              A; Molecule type: mRNA
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A; Molecule type: protein A; Expedimental source: Burkitt lymphoma cell line Raji C; Genetics:
                 A; Reference number: A60771; MUID: 89093941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: I48854
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: MRNA
A; Residuces: 1-459 - REBS-
A; Residuces: 1-459 - REBS-
A; Cross-references: EMBL: X76401; NID:9433830; PIDN: CAA53981.1; PID:9433831
C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F; 151-188/Domain: NGF receptor repeat homology <a href="https://doi.org/10.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087/phi/lib.1087
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R; Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A; Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A; Reference number: I48854; MUID:95178848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                         121
                                                                                                                                                                                                                                 145
                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                              67 YLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA--AWALECTHCELLSDC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 QFRICLSCSSCSTDQV----ETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 PPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDT 181
           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 PYKPEPGYECQISQ-EYYDRKAQMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
                                                                                                                                                                                         90 QFRTCLSCSSCTTDQV----EIRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKC
PYKPEPGYECQISQ-EYYDRKAQMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWN
                                                                                                              67 YLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA--AWALECTHCELLSDC
                                                                                                                                                                                                                                                                                                                                    122 PPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENGGLVEAAPGTAQSDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.54
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 TCKNPLEPLPPEMS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 VC----APESPTLS 210
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g
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Map position: 20q12-20q13.2

C; Superfamily: CD27 antigen; NGF receptor repeat homology

C; Superfamily: CD27 antigen; NGF receptor repeat homology

C; Superfamily: CD27 antigen; NGF receptor surface antigen; transmembrane prot

E; 1-20/70main: signal sequence #status predicted <SIG>

E; 21-27/7Product: B-cell activation protein CD40 #status experimental <MAT>

E; 21-137/7Product: B-cell activation protein CD40 #status experimental <MAT>

E; 144-215/7Domain: transmembrane #status predicted <PTM>

E; 144-215/7Domain: intracellular #status predicted <PTM>

E; 153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A46476
B cell-associated surface molecule CD40, long splice form - mouse
B cell-associated surface molecule CD40, long splice form - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mas musculus (house mouse)
C; Accession: A46476; A46515
B; Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-625, 1992
A; Title: Differential increase of an alternatively polyadenylated mRNA species of mur A; Reference number: A46476; MuID:92105763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A) Note: sequence extracted from NCB1 backbone (NCBIN:75206, NCBIP:75207)
A) Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
A) Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
B) Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay J. Immunol. 149, 3921-3926, 1992
A) Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A) Reference number: A46515; MUID:93094586
A) Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 YLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 PPTA----CR--EKQYLINSQ--CCSLCQPGQKLVSDCTEFTETETECLPCGESEFLDTWN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 PPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 AELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 278; DB 2; Length 277;
Pred. No. 4e-14;
0; Mismatches 83; Indels
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A Note: sequence extracted from NCBI backbone (NCBIP:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD2 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology
A,Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
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35.0%; Pred
tive 20;
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A; Residues: 1-287, 'LV' <GRI>
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Best Local Similarity
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A; Residues: 1-305 <TOR>
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Length 305;

Score 243.5; DB 2; Pred. No. 1.7e-11;

21.5%; 31.0%;

Length 271;

DB 2;

Indels

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C;Superfamily: CD27 antigen; NGF receptor repeat homology C;Keywords: growth factor receptor; transmembrane protein F:1-19/Domain: signal sequence #status predicted <SIG>F:20-271/Product: 0X40 antigen #status predicted <NMT>F:211-235/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                Query Match 19.6%; Score 222.5; DB 2
Best Local Similarity 32.1%; Pred. No. 6.1e-10;
Matches 53; Conservative 17; Mismatches 68
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Best Local Similarity 31.7%
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs tresia, activates a cell death and/or survival signaling cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      positive T lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #status predicted <ECL>
        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          death receptor-6 - chicken
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Species: Onvo-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C; Accession: JC7705
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A; Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A; Reference number: JC7705; MUID:21308433; PMID:11414698
A; Accession: JC7705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N'Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30.Sep.1993 #sequence_revision 30.Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
                                                                                                                                                                                                                                                   RPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPG----TEAEL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTSKRKTQCRCQPGMF-----CAAWALECTHCELLSDCP-----PGTEAELKDEVGKG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 LICDKCPAGTYVSKHCTKSTLRECSPCPDGTFTKHENGIERCHPCRKPCE--LPMIEKTH 107
        Gaps
                                                                                        TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC 74
                                                                                                                                                                   25 TCSD--KQYLHDGQ--CCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 ICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCR-PCDPVMGLEEIAP 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rivallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A; Title: Characterization of the MRC OX40 antigen of activated CD4 positi
A; Reference number: S12783; MUID:90214614
A; Reference number: mRNA
A; Molecule type: mRNA
A; Residues: 1-271 < MAL>
A; Residues: 1-271 < MAL>
A; Residues: BEBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 NNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | | | | | : | :| | | :| | | :| | | | :| | | | :| | | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | 
            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding
F;32-350/Domain: transmembrane #status predicted <PRMY-
F;310-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted
        81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
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        Mismatches
        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Molecule type: mRNA
A, Residues: 1-651 <BRI>
A, Cross-references: GB: AF349908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.09
Best Local Similarity 28.89
Matches 49; Conservative
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OX40 antigen precursor - rat
        54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: dr-6
        Matches
                                                                                        15
                                                                                                                                                                                                                                                                                                                                   81
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Jeas to 240 protein - mouse

N; Alternate names: OX40 antigen

N; Alternate names: OX40 antigen

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Accession: 148700; 148334; S34377

R; Calderhead, D.M.; Bulhanan, J.E.; van den Bertwegh, A.J.; Claassen, E.; Noelle, R.J.

J; Immunol. 151, 5261-5271, 1993

A; Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell

A; Reference number: 148700; MUID: 94044750

A; Reference number: 148700

A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residues: 1-272 <RES>

A; Cross-references: EMBL: 221674; NID: 9312827; PIDN: CAA79772.1; PID: 9312828

R; Rirkeland, M.L.; Copeland, M.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.

Eur. J: Immunol. 25, 926-930, 1995

A; Reference number: 148334; MUID: 95255413

A; Reference number: 148334; MUID: 95255413

A; Residues: 1-14, 'G', 16-272 <RES>

A; Cross-references: EMBL: X83214; NID: 9732818; PIDN: CAA59476.1; PID: 9732819

C; Genetics of the mouse procession of the mouse homologue of rat ox cross-references: EMBL: X85214; NID: 9732818; PIDN: CAA59476.1; PID: 9732819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                81 MGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHC 140
                                                                                                                                                                                                                        -----PGTQPR-QDSSHKLGVDC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 MGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHC 140
                                                                    85
21 KEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 KEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPV 80
                                    28 KDIYPSGHK-CCRECQPGHGMVSRCDHTRDIVCHPCEPGFYNEAVNYDT-CKQCTQCNHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 VPCKAGHFQNTSSP--SARCQPHTRCENQGLVEAAPGTAQSDTTCKN 185
                                                                                                                                                                                                                                                                                                                                                            123 VPCPPGHFSPGSNQA--CKPWTNCTLSGKQIRHPASNSLDIVCED 165
                                                                                                                                                                                                                                                                                                        141 VPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C; Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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31.7%; Pred. No. 2.5e-09;
iive 16; Mismatches 67
                                                                                                                                                                                                                            86 SGSELKONCIPTEDIVCOCR-----
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A; Molecule type: protein
A; Residues: 41-60 <GAT>
A; Residues: 41-60 <GAT>
A; Experimental source: cancer patient serum
R; Olsson, I.; Lantz, M.; Milsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A; Title: Isolation and characterization of a tumor necrosis factor binding protein fr
A; Reference number: A60594; MUID:89171156
A; Accession: A60594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kajihara, J:; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A;Title: Amino acid Sequence of natural tumor necrosis factor alpha inhibitor purifie
A;Reference number: JC2404; MUID:95128033
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F;30-211/Domain: extracellular #status predicted <EXT>
F;30-210/Product: TWF binding protein 1 (tumor necrosis factor alpha inhibitor) #stat
F;41-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid segu A;Reference number: A60231; MUID:90292116
                                                                                                                                              A; Residues: 41-43, 7X, 45-53, 7X, 55-57 <SEC>
R; Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A; Title: Purification and characterization of an inhibitor (soluble tumor necrosis fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 41-43, X', 45-53, V', 55-57, XK', 60 <0LS>
A; Residues: 41-43, X', 45-53, V', 55-57, XK', 60 <0LS>
A; Experimental source: renal failure patient urine
B; Engelmann, H.; Novick, D.; Wallach, D.
D Biol. Chem. 265, 1331-1536, 1990
A; Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden
A; Reference number: A35010; MUID:90110215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Reywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <NEM>
F;215-535/Domain: intracellular #status predicted <NEM>
F;23-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRHCLSCSKCKKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSL---CLNG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEAELKDEVGKGNNHCVPCKAGHF--QNTSSPSARCQPHTRCENQGL--VEAAPGTAQSD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 LTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWA---LECTHCELLSDCPPG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 DQEK-----EYYEPQHR-ICCSRCPPGTYVSAKC-SRIRDTVCATCAENSYNEHWNY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Rosidues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Rosidues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNF-alp'
C;Comentics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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Pred. No. 7.3e-09;
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                                                                                                                                                                                                                                                                                                                                              A; Reference number: A38258; MUID:91062364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 41-45 <ENG>
A; Experimental source: normal urine
R; Kajihara, J:: Assada
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                                                                                                                  A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A38258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A35010
A; Molecule type: pro
                                                                             A; Accession: A60231
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        Numberosis factor receptor 1 precursor (validated) - human
Numberosis factor receptor 1 precursor (validated) - human
Numberosis factor receptor 1 preceptor; Nr Preceptor type 1
Nr Contains the mane service and a factor receptor; Two receptor type 1
Nr Contains the mane service and a factor receptor; Two receptor type 1
Nr Contains a factor receptor a phala inhibitor; tumor necrosis factor binding protein
Craccession: A38008, A3809; A34000, A36555; A380281; S12057, J70758; A60231; A38
R. Fuchs, P. : Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P. P.
A. Title: Structure of the human rwF receptor 1 (p60) gene (TNRF1) and localization to chancession: A38008, MUD:92250049
A. Notecule type: DNA
A. N
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A;Residues: 1-455 <GRA>
A;Cross-references: GB:M37764
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R;Nophar, Y:, Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
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A;Reference number: $12057; MUID:91006021
A;Accession: $12057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ne
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A;NOte: parts of soluble TNF binding protein 1, including its amino and carboxyl ends,
R;Kemper, O.; Wallach, D
Gene 134, 209-216, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Cloning and partial characterization of the promoter for the human p55 tumor A;Reference number: JT0758; MUID:94085779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G.; Wingfield, P.; Dayer, J.M.
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A; Residues: 1-13 < KENA
A; Seckinegr. P.; Vey. E.; Turcatti, G
Eur. J. Immunol. 20, 1167-1174, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-455 <NOP>
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Gaps

23;

84;

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Length 455; Indels

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GSE protein - variola minor virus (strain García-1966)
C;Species: variola minor virus
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession: D72175
R;Shochelkunov, S.N.; Tormenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lo submitted to GenBank, March 1998
A;Bescription: Analysis of the complete coding sequence of DNA of alastrim variola mi A;Reference.number: A72150
A;Recession: D72175
A;Accession: D72175
A;Molecule type: DNA
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759 A;Experimental source: strain Garcia-1966 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 LTICQLCR-PCDPVMGLEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 LPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKC--GI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTICQLCR-PCDPVMGLEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 PYTPPNGKCKDTEYK----RHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNH
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                  A; Molecule type: DNA
A; Residues: 31-168 <SHC>
A; Residues: 31-168 <SHC>
A; Cross-references: EMBL:x69198
A; Experimental source: strain India-1967, ssp. major
C; Genetics:
C; Genetics:
C; Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F; 32-66/Domain: NGF receptor repeat homology <NG2>
F; 68-109/Domain: NGF receptor repeat homology <NG2>
F; 110-151/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                     Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 349;
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                                                                                                                                                                                                                                                                                                                                                                                 18.5%; Score 210; DB 2; 29.0%; Pred. No. 6.5e-09; tive 20; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.3%; Score 207; DB 2; 29.0%; Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 EAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYGVSGHTSVGDVICSPCGFGTYSHTVSSADKCEP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQP 160
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Matches 45; Conserv
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nes 45; Conserv
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532385
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Best Local S:
Matches 45;
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   A; Accession:
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                                                                                                                                                                                                                                                                                       C; Species: variola major virus
C; Species: variola major virus
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C; Accession: T28623
R; Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin Nature 366, 748-751, 1993
A; Title: Potential virulence determinants in terminal regions of variola smallpox virus A; Reference number: 220488; MUID:94088747
A; Accession: T28623
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: DNA
A; Residues: 1-348 < AMS>
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A.Experimental source: strain India-1967, ssp. major, isolate Ind3
A.Experimental source: strain India-1967, ssp. major, isolate Ind3
R.Koltykalov, A.B. Blinov, V.W.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frol submitted to the EMBL Data Library, April 1999
A.Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P. A.Reference number: $46868
A.Reference number: $46868
A.Status: preliminary
A.Residues: preliminary
A.Residues: 1-349 < KOL>
A.Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A.Residues: atrain India-1967, isolate Ind3
R.Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
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A;Reference number: S32385, MUID:93202281
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
S*Blinov, V.M.
submitted to GenBank, November 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60933.1; PID:9439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
153 TVHLSCQE--KQNTVCT-CHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 LTICQLCR-PCDPVMGLEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 IPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKC--GI 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 EAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQP 160
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                                                                                                                                                                                                                                                              hypothetical protein G2R - variola major virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: B28R protein (COP)
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A; Accession: D36858
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A; Residues: 1-349 <BLI>
                                                                                                      210 TTVLLPL 216
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                                                           181 TTCKNPL 187
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86 IAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKA 145
                                                                                                                                 GHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC--KNPLEPLPPEMSG 196
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Fig. J. Immunol. 24, 677-683, 1994
A; Fitle: The human OX40 homolog: cDNA structure, expression and chromosomal assignment characteristics number: 137552; MUID:94170844
                     Risuter, B.; Pauli, U.
Gene 183, 263, 286, 1995
A.Title: Cloning of the CDNA encoding the porcine p55 tumor necrosis factor receptor.
A;Reference number: JC4302; MUID:96011645
                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor 1.29/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;84-126/Domain: NGF receptor repeat homology <NGF>
F;211-231/Domain: transmembrane #status predicted <TMM>
F;361-447/Domain: signal transduction #status predicted <SIT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 TE----AELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQ-- 178
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A;Residues: 1-277 <RES>
A;Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:9472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology
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A;Accession: PC4093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.2%; Score 206; DB 2; 29.4%; Pred. No. 1.6e-08; iive 22; Mismatches 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44-82/Domain: NGF receptor repeat homology <NG1>
                                                                                                                                                                                                                                                      A;Wolecule type: protein
A;Residues: 1-7 <SU2>
A;Experimental source: kidney cell line 15
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Best Local Similarity 29.44
Matches 57; Conservative
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C; Accession: JC4302; PC4093
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Best Local Similarity
                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-461 <SUT>
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		38	128
OM protein - protein search, using sw model		39	126
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Scoring table:	Searched:	Total number of

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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T10A_HUMAN TR12_HUMAN LMAS_HUMAN LMA1_MOUSE TNR7_HUMAN LMA5_MOUSE LMA5_MOUSE DLL1_RAT PCKS_HUMAN PCKS_BRACL PGBM_MOUSE
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11-JUN 1994 (Rel. 2), Last sequence update 16-OCT-2001 (Rel. 40, Last annotation update) Imphotoxin-beta receptor precursor (Tumo 2 method protein) (Tumor necrosis factor LTMP of TWERSF3. LTBR OR TWECR OR TWERSF3. ENARTH, SELLOS (Grandata; Craniata; V Mammalia; Eutheria; Primates; Catarrhini; NCBL_TAXID-9606; [1] SEQUENCE FROM N.A. TISSUE-Liver N.A. TISSUE-Liver N.A. TISSUE-Liver N.A. Construction and evaluation of a hncDNA (Construction and evaluation of a media some denoies 16:214-218(1993). EUNCTION. MEDLINE-94255209; Pubmed-8171323; FUNCTION. MEDLINE-94255209; Pubmed-8171323; FUNCTION. MEDLINE-94255209; Pubmed-8171323; FUNCTION. TAY SECREPTOR FOR THE LYMPHOTOXI I MEDLINE-9425520; THIS SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinformatics by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (Seor send an email to license send send send send send send send	ate) r necrosis factor receptor . C receptor). ertebrata; Euteleostomi; Hominidae; Homo.
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SIGNAL
 SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.0%; Score 771; DB 1; 70.7%; Pred. No. 6.7e-59; ive 14; Mismatches 40;
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                                                                                                                                                                 MGD; MGI:104875; Ltbr.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
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                                                                                                                         EMBL; U29173; AAA68964.1; -.
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Best Local Similarity 70.7%
Matches 135; Conservative
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4115
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"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
and expression.";
                                                                                                                                                                                                                                                                   1 SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
                                                                                                                                                                                                                                                                               28 SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDIVCATCAENS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
624626E6022F656F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-96163885; Pubmed-8586432;
Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.
                                                                                                                                                                                                                                                Indels
 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                        100.0%; Score 1133; DB 1;
100.0%; Pred. No. 9.4e-90;
iive 0; Mismatches 0;
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01-0cT-1996 (Rel. 34, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
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TNFR-CYS 2.
TNFR-CYS 3.
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                                                                                                                                                                                         46709 MW;
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Best Local Similarity
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              REPUBLICATION OF THE PROPERTY AND DEPTHENCE OF THE PROPERTY OF
01-AUG-1991 (Rel. 19, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor binding protein 2) (IPPII) (P80) (TNF-R2) (P75) (CD120B) (Etanercept).
TNFRSFIB OR TNFR2 OR TNFR2
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-90260639; PubMed-2160731;
Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
Dower S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins.";
Science 248:1019-1023(1990).
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MEDLINE-93016040; PubMed-1328224;
Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
Lipari M.T., Goeddel D.V.;
"Biochemical properties of the 75-kDa tumor necrosis factor receptor.
Characterization of ligand binding, internalization, and receptor
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MEDLINE-90110215; PubMed-2153136;
Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface
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MEDLINE-91056048; PubMed-2173696;
Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.", Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
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Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
"Structural basis for self-association and receptor recognition of
human TRAF2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Physical mapping and genomic structure of the human TNFR2 gene."; Genomics 35:94-100(1996).
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96299745; PubMed=8661109;
Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J., Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91045991; PubMed=2172983;
Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
A second tumor necrosis factor receptor gene product can shed naturally occurring tumor necrosis factor inhibitor.";
Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
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MEDLINE-90349572; PubMed-2166946;
Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
Ringold G.M.;
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J. Biol. Chem. 265:1531-1536(1990).
                                                                                                                                                                       Homo sapiens (Human)
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Nature 398:533-538(1999).

-! FUNCTION: FREEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

-! SUBCELLULAR LOCATION: Type I membrane protein.

-! FTM: BHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to servere rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNFR2 linked to an Immuglobulin Fc chain. It binds to TNF-alpha and blocks its interactions with receptors.
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TUFF-CYS 2.
TUFF-CYS 3.
TUFF-CYS 3.
TUFF-CYS 4.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 4 TNFR-CYS REPEARS.
DATABASE: NAME-PROW; NOTE=CD guide CD120b entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd120b.htm".
DATABASE: NAME-Enbrel; NOTE=Clinical information on Enbrel;
WWW-"http://www.enbrelinfo.com/".
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EMBL; U52161; AAC50622.1; JOINED.
EMBL; U52162; AAC50622.1; JOINED.
EMBL; U52163; AAC50622.1; JOINED.
EMBL; U52164; AAC50622.1; JOINED.
EMBL; M55994; AAA36755.1;
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BMBL; U52157; AAC50622.1; JOINED.
EMBL; U52158; AAC50622.1; JOINED.
EMBL; U52159; AAC50622.1; JOINED.
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SM00208; TNFR; 4.
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PIR, A36007; A36007.
PIR, A36475.
PIR, B35010; B35010.
PIR, A23666; A23666.
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TR11_MOUSE
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                                                                                                                                                                   HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                           Gaps
                                                                                                                                     28 AFTPYAPEPGSICR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQ 85
                                                                                                                         5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 . .) (POTENTIAL)
                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91187985; PubMed=1849278;
Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
Wong G.H., Chen E.Y., Goeddel D.V.;
"Cloning and expression of cDNAs for two distinct murine tumor
necrosis factor receptors demonstrate one receptor is species
specific.";
                                                                           26.9%; Score 305; DB 1; Length 461; 35.0%; Pred. No. 4.1e-19;
                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
receptor 2 precursor (TNF-R2) (p75).
                                                                                                   78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kissonerghis M., Fellowes R., Feldmann'M., Chernajovsky Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacob C.O., Liu J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
          -> P (IN REF. 4).
-> M (IN REF. 1 AND 3).
-> T (IN REF. 4).
603B580ECD67636F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
N-LINKED (GLCNAC. .
R -> P (IN REF. 4).
R -> M (IN REF. 1 A
A -> T (IN REF. 4).
                                                                                      4.1e-19;
                                                                                                                                                                                                                                                                                                                                      474 AA.
                                                                                                  24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=91246168; PubMed=1645445;
                                                                                                                                                                                                                                                                                                                                   TRIB_MOUSE STANDARD; F
P25119; P97893;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                         GTAQSDTTC--KNPLEPLPP 192
                                            .
Σ
                                                                                                                                                                                                                                                                              192 GNASRDAVCTSTSPTRSMAP 211
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                                 363
48316
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                                                                                                   Conservative
193
141
196
                                                                                                                                                                                                                                                                                                                                                                                             Tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
193
141
196
363
461 AA;
                                                                                       Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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CARBOHYD
CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 YLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA--AWALECTHCELLSDC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 QFRTCLSCSSSCTTDQV----EIRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 PPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR NECROSIS FACTOR RECEPTOR 2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 474;
                                                                                                                        EMBL; M60469; AAA39752.1; -.

R EMBL; M59378; AAA40463.1; -.

R EMBL; W39488; AAA60512.1; -.

R EMBL; U39488; AAA65021.1; -.

R EMBL; U39488; AAA65018.1; -.

R EMBL; W3128; CAA66618.1; -.

R PIR; B38634; B38634.

R MGD; MGI:1314883; INFR.eftb.

R DFGM; PD00020; TNFR.ef; 4.

R PCODOM; PM00208; TNFR.ef; 4.

R PCOMOR; SM00208; TNFR.ef; 1.

R PROSITE; PS00652; TNFR.NGFR.1; 2.

R PROSITE; PS00652; TNFR.NGFR.2; 3.

R RCCEPTOR; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINKED (GLCNAC. . .) (P. 462EAE398C4D6563 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.0%; Score 295; DB 1; 34.0%; Pred. No. 3e-18; ive 24; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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035305;
16-0CT-2001 (
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01-MAR-2002 (
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66621 MW; F8C1872E99511D8E CRC64;

625 AA;

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                                                                                                                                                                                                                                                                                                                                                    "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
Jumius necrosis factor receptor superfamily member 11A precursor
(Receptor activator of NF-KB) (Osteoclast differentiation factor
receptor) (ODFR).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                       TISSUE-Fetal liver;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Transmembrane; Repeat; Signal.

1 30 POTENTIAL.
31 625 TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUPERFAMILY MEMBER 11A. EXTRACELLULAR (POTENTIAL).
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99097247; PubMed=9878548;
                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1314891; Thfrsflla.
InterPro: IPR001368: TNFR_c6.
Pfam. PF00020; TNFR_c6; 3.
ProDom: PD00071; TNFR_c6; 1.
SMART; SM00208; TNFR, 4.
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                                                                                TNFRSF11A OR RANK.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                      Galibert L.;
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SIGNAL
CHAIN
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Boloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Balley J., Barlow K.F., Bartes K.N., Bearde D.M.,
Beasley O.P., Bird C.P., Blakes K.B., Beridgeman A.M., Brown A.J.,
RA Chapman J.C., Clanma M., Clark G., Clark L.N., Clark S.T., Clee C.M.,
RA Clegs S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
Ra Lington A., Crankland J.A., Fraser A., French L., Garner P.,
RA Brington A.G., Frankland J.A., Fraser A., Honden P.J.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Grafham D.V., Griffiths C., Griffiths A., Laird G.K., Lawlor S.,
Lehvaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA MINE S., Mistry D., Moore M.J., McConnachle L.J., McCapt A.J.,
RAILI Mancre B.J.C.T., Prathalingam S.R., Pluub R.W., Ramsay H.,
Ran M.L., Soderlund C., Steward C.A., Sulston J.E.,
Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Ryanney A., Tromans A.C., Vaudin M., Wallis J.W.,
Rhitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Ryanning L., Wray P.W., Hubbard T., Durbin R.W., Bentley D.R., Beck S.,
Ryanning L., Wray P.W., Hubbard T., Durbin R.W., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                         64 HWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                              GTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENGGLVEAAPGTAQSDTTC 183
                                                                              Gaps
                                                                                                                                              4 QAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
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                                                                                                                                                                                                                     30 QVTPPCTQE-----RHYEHLGR-CCSRCEPGKYLSSKCTPTSDSVCLPCGPDEYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Last sequence update)
01-MAK-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (Bp50) (CDw40).
   Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=89356608; PubMed=2475341;
Stamenkovic I., Clark E.A., Seed B.;
A B-lymphocyte activation molecule related to the nerve g factor receptor and induced by cytokines in carcinomas.";
EMBO J. 8:1403-1410(1989).
                                                                          85; Indels
   DB 1;
Score 283; DB 1,
Pred. No. 4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 AA.
                                                                       25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last seq
01-MAR-2002 (Rel. 41, Last ann
25.0%;
32.6%;
                                                                          Conservative
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                                         Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 SSSM 199
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       Query Match
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67 YLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTE 126

127 AELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183

22 PPTA-----CR--EKQYLINSQ--CCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWN 72

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                                                                                                                              MEDLINE-98264353; PubMed-9605317;
Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M.,
Sheng Z., Naismith J.H., Thomas D.;
The role of polar interactions in the molecular recognition of CD40L
with its receptor CD40.";
Protein Sci. 7:1124-1135(1988).
I- FUNCTION: RECEPTOR FOR A CYTOKINE LICAND KNOWN AS CD40L.
I- SIMCLAGIN: RECEPTOR FOR A CYTOKINE LICAND FORCINOMAS.
I- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
I- SIMILARITY: CONTAINS 4 TWRR-CYS REPEATS.
I- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
                                                                  of
                                                              "Construction and analysis of a detailed three-dimensional model the ligand binding domain of the human B cell receptor CD40."; Proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
BC8776EC2C4A5680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
Probom; PD000771; TNFR_c6; 1.
SMART; SM0208; TNFR, 4.
PROSITE; PS00625; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 4.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                      3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
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TNFR-CYS 2.
TNFR-CYS 3.
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                                       MEDLINE=97189482; PubMed=9037712;
                          3D-STRUCTURE MODELING OF 24-144
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PDB; 1CDF; 01-APR-97.
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Nature 414:865-871(2001).
                                                    Bajorath J., Aruffo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
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familial expansile osteolysis.";
Nat. Genet. 24:45-48[2000).
-!- Genet. 24:46-48[2000).
-!- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS
OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTTAL FOR RANKL-
MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF
INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: UBLOUITOUS EXPRESSION WITH HIGH LEYELS IN
SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT FEO 16-L--L-21 DUPL, VARIANT PDB2 13-A--L-21 DUPL, AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLAND.

GLAND.

JESASE: DEFECTS IN TNFRSF11A ARE THE CAUSE OF FAMILIAL EXPANSILE OSTEGASE: DEFECTS (FEQ), A RARE AUTOSOMAL DOMINANT BONE DISORDER CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING. THE STEDARCTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING THE ADMILTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFHESS AND LOSS OF DENTITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE: DEFECTS IN THERSFILA ARE A CAUSE OF FAMILIAL PAGET DISEASE DE BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDB2). IT AS A BONE REMODELLING DISCADER WHITH CLINICAL SIMILARITIES TO FEO. UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galibert L.;
"A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
Nature 390:175-179(1997).
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Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano
Morinaga T., Higashio K.;
"RANK is the essential signaling receptor for osteoclast
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 11A precursor Receptor activator of NF-KB) (Osteoclast differentiation factor receptor) (OPFN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson D.M.; "Mutations in TNFRSF11A, affecting the signal peptide of RANK,
                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Dendritic cell;
MEDLINE-9803-2977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hughes A.E., Raiston S.H., Marken J., Bell C., MacPherson H., Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentiation factor in osteoclastogenesis.";
Biochem. Biophys. Res. Commun. 253:395-400(1998).
                                                                                                                   616 AA
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                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                      TR11_HUMAN
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                                                                                                TR11_HUMAN
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5

Gaps

12;

24.5%; Score 278; DB 1; Length 277; 35.0%; Pred. No. 5.2e-17; ive 20; Mismatches 83; Indels

Conservative

62;

Best Local Matches 6

Similarity

Query Match

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HSSP; P25942;
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TRANSMEM
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SEQUENCE
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TNR5_BOVIN
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                               Receptor; Glycoprotein; Transmembrane; Repeat; Signal; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
ALLLLCALL -> ALLLLCALLLCALL (IN
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                                                                                                                                                                                                         TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.4%; Score 277; DB 1; Length 616
31.7%; Pred. No. 1.3e-16;
ive 28; Mismatches 87; Indels
                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                   'FTId=VAR_011518.
E3DE9A7A08196F81 CRC64;
                                                                                                                                                                                                                                 POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                  FTIG=VAR_011516
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-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                   EMBL; AF018253; AAB86809.1; -.
HSSP; P25942; 1CDF.
                                                                                                                           InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
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                                                                                                                                                      SMART; SM00208; TNFR; 4.
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                                                                                                                                                                                         Disease mutation.
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MIM; 174810;
MIM; 602080;
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DOMAIN
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TURE CYS 2.

TURE CYS 3.

TURE CYS 3.

TURE CYS 4.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97281252; PubMed-9135560;
Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and biological function of the bovine CD40
homologue: role in B-lymphocyte growth and differentiation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00652; TURE NGFR 1; 1.
PROSITE; PS50050; TUFR NGFR 2; 1.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 1 19 POTENTIAL.
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                                                                                                                       member 5 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunology 90:294-300(1997).
--- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
--- SUBCELLULA: LOCATION: Type I membrane protein.
--- SIMILARITY: CONTAINS 4 INFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                 (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
INFRSF5 OR CD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUPERFAMILY MEMBER 5
                                                                        01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily me
     AA.
  269
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                                                   (Rel. 35, Created)
(Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U57745; AAC48710.1; -. HSSP; P25942; 1CDF.
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215
>269
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SMART; SM00208; INFR;
                                                                                                                                                                                                     Bos taurus (Bovine).
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TNR5_BOVIN
Q28203;
01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
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20 EKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDP 79

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                    86 NIGLRIQSEGTLNTDTICVCVEGQHCTSHT--CESCTPHSLCLPGFGVK---QIATGLLD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genomic structure and chromosomal mapping of the murine CD40 gene."; J. Immunol. 149:3921-3926(1992).
                                   80 VMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKG--N 137
            82
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-92105763; PubMed=1370315; Torses R.M., Clark E.A.; Torses R.M., Clark E.A.; "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation."; J. Immunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00208; TNFR; 4. PROSTE; PSO0652; TNFR_MOFE_1; 1. PROSTEE; PSO0652; TNFR_MOFE_1; 1. PROSTEE; PS50050; TNFR_MOFE_2; 4. Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Liver;
STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-93094586; Pubmed-1281194;
Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Torres R.M.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                   138 NHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                       289 AA
                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M94128; AAA37404.1; JOINED.
EMBL; M94127; AAA37404.1; JOINED.
PIR; A46476; A46476.
                                                                                                                                                                                                 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001368; TNFR_c6. Pfam; PF00020; TNFR_c6; 4. ProDom; PD000771; TNFR_c6; 1.
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                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 TCSD--KQYLHDGQ--CCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQH 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUB-cervical adenocarcinoma;
MEDILINE-97053782; PubMed-8898196;
Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
Merpess simplex virus-1 entry into cells mediated by a novel member the TNF/NGF receptor family.";
Cell 87:427-436(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 RPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPG----TEAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Herpesvirus entry mediator) (Tumor necrosis factor receptor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                       -LINKED (GLCNAC. . .) (POTENTIAL). C791CB6D2FEA574E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 TDTV-----CHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 KDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor necrosis factor receptor superfamily member 14 precursor
                                                                                                                                                                                                                                                                                                                                                                                                    Length 289;
TUMOR NECROSIS FACTOR RECEPTOR
                                     EXTRACELLULAR (POTENTIAL).
                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                 SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                  21.5%; Score 243.5; DB 1
31.0%; Pred. No. 4.7e-14;
ive 22; Mismatches 81
                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TR14_HUMAN STANDARD; PRT; 283 AA. 0292955; 09UM65; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY
BY SIMILARITY.
                                                                                            TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                               MW.
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2153
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289 AA;
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                                       DOMAIN
                                                                            DOMAIN
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                                                                                                                                   REPEAT
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271 AA

PRT;

STANDARD;

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165 --- CPP 167
                                                                              01-APR-1990
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                                                         TNR4_RAT
P15725;
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TRANSMEM
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SIGNAL
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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
SEQUENCE FROM N.A.

Zhang W., Wan T., Cao X.;

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: RECEPTOR FOR TURSF14. INVOLVED IN LYMPHOCYTE ACTIVATION.

PLAYS AN IMPORTANT ROLE IN HSV PATHOGENESIS BECAUSE IT ENHANCED

THE ENTRY OF SEVERAL WILDTYPE HSV STRAINS OF BOTH SEROTYPES INTO

CHO CELLS, AND MEDIATED HSV ENTRY INTO ACTIVATED HUMAN I CELLS.
                                                                           SUBCELLULAR LOCATION: Type I membrane protein (Probable).
TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION IN LUNG, SPLEEN, AND THYMUS.
SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 AELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENGGLVEAAPGTAQSDTTCKNP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 YLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 PPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 PCYAPALPSCK--EDEY--PVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
N'LINKED (GLCNAC. . .) (POTENTIAL).
N'LINKED (GLCNAC. . .) (POTENTIAL).
K'-> R (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 283;
                                                                                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
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46CE13C2C70242C1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                          SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.3%; Score 230.5; DB 1
30.1%; Pred. No. 5.9e-13;
iive 13; Mismatches 66
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TNFR-CYS 2.
TNFR-CYS 3.
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                                                                                                                                                                                                                                                                                                                PROSITE; PS50052; TNFR_NGFR_1; 1. PROSITE; PS50050; TNFR_NGFR_2; 2.
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Pfam; PF00020; TNFR_c6; 3.
ProDom; PD00071; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                  EMBL, U70321; AAB58354.1; -. EEMBL, U81232; AAD00505.1; -. EMBL, AF153978; AAF75588.1; -. HSSP; P25942; 1CDF.
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                                                                                                                                                                                                                                                             MIM; 602746
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TRANSMEM
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                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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           01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen) (MRC OX40).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                  Mallett S., Fossum S., Barclay A.N.; "Characterization of the MRC OX40 antigen of activated CD4 positive 1 lymphocytes -- a molecule related to nerve growth factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 KEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPV 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C06465136B16E821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCOMPLETE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBO J. 9:1063-1068(1990).
-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
-i- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
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TNFR-CYS 2.
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TNFR-CYS 4.
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                                                                                                                                                                                                                                                                                                                                           MEDLINE=90214614; PubMed=2157591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X17037; CAA34897.1; -. PIR; SO8036; SO8036. PIR; S12783; S12783. HSSP, P19438; IEXT. Interpro; IPR001368; TNFR_C6. Pfam; PF00020; TNFR_C6; 3. Probom; PD000771; TNFR_C6; 1.
(Rel. 14, Created)
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271 AA;
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                                                                                                                                          (Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
sis factor receptor superfamily member 4 precursor (OX40L
                                                                                                                                                                                                                                                                      MEDLINE-9044750; PubMed=8228223;
Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell activation marker that may mediate
                                                                                                                                                                                                                                                                                                                                                                                              Gene structure and chromosomal localization of the mouse homologue
          ----PGTQPR-QDSSHKLGVDC
                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00652; TWFR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-95255413; Pubmed-7737295;
Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                              141 VPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKN 185
                                            123 VPCPPGHFSPGSNQA--CKPWTNCTLSGKQIRHPASNSLDTVCED 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
TWRR-CYS 1.
TWRR-CYS 2.
TWRR-CYS 3 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Immunol. 25:926-930(1995).

- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                      T-B cell interactions.";
J. Immunol. 151:5261-5271(1993).
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EMBL; X85214; CAA59476.1; --
HSSP; P19438; 1ExT.
MGD; MGI:104512; TDIFSf4.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 3.
ProDom; PD000771; TNFR_C6; 1.
SMART; SM0208; TNFR; 3.
                                                                                                                                (Rel. 33, Created)
receptor) (OX40 antigen).
TNFRSF4 OR TXGP1 OR OX40.
                                                                                                           STANDARD;
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103
124
165
                                                                                                                                                                                                                                                                                                                                                                                                        of rat 0X40 protein.
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SEQUENCE FROM N.A.
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212
237
26
62
62
104
                                                                                                                                                                  Tumor necrosis
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                                                                                                                                01-FEB-1996
                                                                                                                                           01-FEB-1996
16-OCT-2001
                                                                                                          TNR4_MOUSE
P47741;
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TRANSMEM
DOMAIN
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MEDLINE-90235285; PubMed-2158863; Schall T.G., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W., Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.; "Molecular cloning and expression of a receptor for human tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201. MEDLINE=91006021; PubMed=1698610; Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R., Aderka D., Holtmann H., Wallach D.; Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
MEDLINE=91090841; PubMed=1702293;
MEDLINE=91090841; PubMed=1702293;
MEDLINE=91090841; PubMed=1702293;
Minmer A., Maurer-Pogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
"Molecular cloning and expression of human and rat tumor necrosis
factor receptor chain (p60) and its soluble derivative, tumor
necrosis factor-binding protein.";
DNA Cell Biol. 9:705-715(1990).
                                                                                                                                                                                                                                                                                                                                                                                                          81 MGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PGTQPR-QDSGYKLGVDC 123
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                                                                                                                                                                                                                                                                                                                                             86
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                                                                                                                                                                                                                                                                                                                                             29 KHTYPSGHK-CCRECQPGHGMVSRCDHTRDTLCHPCETGFYNEAVNYDT-CKQCTQCNHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor necrosis factor receptor 1 precursor (Tumor necrosis factor binding protein 1) (TBPI) (p60) (TNF-RI) (TNF-RI) (p55) (CD120A). TNFRSFIA OR TNFRI OR TNFAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      . .) (POTENTIAL).
                                                                                                                                                                                                                     31;
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MEDLINE-90235284; PubMed-2158862;
Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
                                                                                                                                                    Length 272;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 VPCPPGHF----SPGNNQACKPWINCTLSGKQIRHPASDSLDAVCED 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 VPCKAGHFONTSSP--SARCQPHTRCENQGLVEAAPGTAQSDTTCKN 185
N-LINKED (GLCNAC. . .) (Po
A -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
                                                                                                                                                                                                                  67;
                                                                                                                                                        DB 1;
                                                                                                                                                    18.9%; Score 214.5; DB 31.7%; Pred. No. 1.3e-11; ive 16; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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144 N.
15 A.
30153 MW;
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EMBO J. 9:3269-3278(1990).
                                                                                                                                                                                                                  53; Conservative
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                                                                                                                                                 Query Match
Best Local Similarity
Matches 53; Conserv
                                                             272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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CARBOHYD
CONFLICT
SEQUENCE
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TR1A_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structure 4:1251-1262(1996).

-!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECEPTOR: THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSCOURT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF NONCYTOCIDAL THE BEFREGIS INCLUDING ANTI-VIRAL STATE AND ACTIVATION OF THE ACID SPHINGOMYELINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBDIVIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THERI LEADS TO MOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERFACE SPECIFICALLY WITH THE DEATH DOMAIN OF TRAND. VARIOUS TRAND-INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FAND, ARE RECRUITED TO TRAIL COMMENS BY THEIR ASSOCIATION WITH TRAND. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.
                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB MEDLINE-93258809; PubMed=8387891;
                                                                                                                                                                                                                                                SEQUENCE OF 41-40.
MEDLINE-9010215; bubMed-2153136;
BEGLINE-9010215; bubMed-2153136;
Brgelmann H., Novick D., Wallach D.;
Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface urine.
                                                                                                                                                                                                                                                                                                                                                                                                         Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
Broger C., Loetscher H., Lesslauer W.;
"Crystal structure of the soluble human 55 kd TNF receptor-human TNF
beta complex: implications for TNF receptor activation.";
Cell 73:431-445(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
MEDILTE=97049483; PubMed-6939750;
Malsmith J.H., Devine T.Q., Khono H., Sprang S.R.;
"Structures of the extracellular domain of the type I tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: THE DOMAIN THAT INDUCES A-SWASE IS PROBABLY IDENTICAL
THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SWASE.
SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.

BATABASE: NAME-PROW: NOTE-CD guide CD120a entry:
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
                                                                    and
                                                                                                                                             MEDLINE-92250049; PubMed-1315717;
Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;
"Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
localization to chromosome 12p13.";
Genomics 13:219-224(1992).
                                                Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.; "Cloning of human tumor necrosis factor (TINF) receptor CDNA expression of recombinant soluble TNF-binding protein."; Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
                                                                                                                                                                                                                                                                                                                             nor necrosis factor receptors.";
Biol. Chem. 265:1531-1536(1990).
SEQUENCE FROM N.A.
TISSUE-placenta;
MEDLINE-91017509; PubMed-2170974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X55313; CAA39021.1; -.
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                                                                                                                                   SEQUENCE FROM N.A.
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EMBL;
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TUMOR NECROSIS FACTOR RECEPTOR 1.
TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWA---LECTHCELLSDCPPG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 TEAELKDEVGKGNNHCVPCKAGHF - QNTSSPSARCQPHTRCENQGL - VEAAPGTAQSD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQEK------EYYEPQHR-ICCSRCPPGTYVSAKC-SRIRDTVCATCAENSYNEHWNY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis; 3D-structure; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
P -> T (IN DBSNP:1804532).
                                                                                                                                                                                                                                                                                                                                                                                                                       THER-CYS 1.
THER-CYS 2.
THER-CYS 3.
THER-CYS 4.
N. SWASE ACTIVATION DOMAIN (NSD).
DEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4CEFBA96D03B8225 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_011813.
MISSING (IN REF. 4).
GPAA -> APP (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.6%; Score 210.5; DB 32.6%; Pred. No. 4.6e-11 tive 19; Mismatches 8
", M63121; AAA36754.1; -.
", M78866; AAA61201.1; -.
", M78864; AAA61201.1; JOINED.
", M78865; AAA61201.1; JOINED.
", M60275; AAA36756.1; -.
                                                                                                                                                                                                                                                                               PROSITE; PS00652; TNFR_NGFR_1; 3. PROSITE; PS50050; TNFR_NGFR_2; 3. PROSITE; PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50494 MW;
                                                                                                                                                                                    InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_C6.
                                                                                                                                                                                                              Pfam: PF00531; death: 1.
Pfam: PF00020; TNFR_c6; 4.
Probom: PD000071; TNFR_c6; 1.
SMART: SM00005; DEATH: 1.
SMART; SM000208; TNFR: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                    1TNR; 31-JUL-94.
1NCF; 07-DEC-95.
1EXT; 11-JAN-97.
                                                                                 A34899; GQHUT1.
A35010; A35010.
                                                                                                         S12057.
A38208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 455 AA;
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                                                                                                                                                                                                                                                                                                                                                              22
41
22
23
23
23
23
43
43
11
16
16
33
83
33
83
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A38208;
                                                                                                                                                                            MIM: 191190;
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                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
153 TVHLSCQE--KQNTVCT-CHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSG 209
                                                                                                                                                                                                                                                                                                                                                                              Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.; "Genes of variola and vaccinia viruses necessary to overcome the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 LTICQLCR-PCDPVMGLEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 PYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 PYTPPNGKCKDTEYK----RHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNH 79
                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                           protective mechanisms.";
FEBS Lett. 319:80-83(1993).
-1- SIMILARITY: CONTAINS 2 THFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 210; DB 1; Length 349;
Pred. No. 4e-11;
); Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 TNFR-CYS 1.
108 TNFR-CYS 2.
38189 MW; D45D40B5C6F780EF CRC64;
                                                                                                                                                                              (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                     349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 EAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYGVSGHTSVGDVICSPCGFGTYSHTVSSADKCEP 170
                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                STRAIN-INDIA-1967 / ISOLATE IND3;
MEDLINE-93202281; PubMed-8384129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00652; TNFR_NGFR_1; 2. PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.5%; Scoi
29.0%; Pred
tive 20; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P25942; ICDF.
InterPro; IPRO1368; TNFR_c6.
Pfam, PF00020; TNFR_c6; 2.
Procom; P0000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X69198; CAA49137.1; -. EMBL; X67117; CAA47540.1; -. PIR; D36858. D36858. PIR; S35987. PIR; S46888; S46888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                            Protein C22/B28 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31
67
349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        Orthopoxvirus.
NCBI_TaxID=10255;
                                            181 TTCKNPL 187
                                                              || || ||
210 TTVLLPL 216
                                                                                                                                                                                                                                                          Variola virus.
                                                                                                                                                                                 01-FEB-1994
                                                                                                                                                                                              01-FEB-1994
16-OCT-2001
                                                                                                                                                   VC22_VARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                           Suter B., Pauli U.H.;

"Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
receptor.";

Gene 163:263-266(1995).

-I- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
GEGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
RECRUITS CASPASE-8 PROTECLIVIC ACTIVATION WHICH INITIATES THE
SUBSEQUENT CASCADE OF CASPASES (ASPATATE-SPECIFIC CYSTEINE
RECRUITS CASPASE) PROTECLIVIC ACTIVATED WHICH INITIATES THE
SUBSULIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD. INTERACTING
WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD. INTERACTING
WITH THE DEATH AS TRAFS, RIP AND POSSIBLY FADD. THIS COMPLEX
ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
NP-KAPPA B SIGNALING (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: TYPE I membrane protein.

-I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                               01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-RI)
                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Procerty, frontable intrace.

Prodon: PF00030; death; language and peroces.

Prodon: PF00020; TNFR_c6; 3.

Prodon: PD00071; TNFR_c6; 1.

SMART: SM00005; DEATH; 1.

SMART: SM00208; TNFR_NGFR_1; 3.

PROSITE; PS00652; TNFR_NGFR_1; 3.

PROSITE; PS50017; DEATH_DOMAIN; 1.

Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.

SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.

TNFR-CYS 4.

N-SMASE ACTIVATION DOMAIN (NSD).

DEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. CYTOPLASMIC (POTENTIAL).
 461 AA.
 PRT;
                                                                                                                                                                                                                                              MEDLINE=96011645; PubMed=7590278;
                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U19994; AAC48499.1; -.
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
461
210
2233
2233
461
125
1166
1195
447
                                (Rel. 34, (Rel. 34, (Rel. 40,
                                                                                                                                Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P19438; 1TNR.
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                   (p55).
TNFRSF1A OR TNFR1.
                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                  TISSUE=Kidney;
                                01-0CT-1996
01-0CT-1996
TR1A_PIG
P50555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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Fri Oct

Search completed: October 4, 2002, 10:15:23 Job time: 241 sec

202 NDFQDTGTTVLLPL 215

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October 4, 2002, 10:11:47; Search time 26.58 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                              OM protein - protein search, using sw model
                                                                                                                                                  Run on:
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(Without alignments) 1282.167 Million cell updates/sec	SEPTICK NPL EPL PPEMSGT 197	
(W1 128	US-09-299-139A-1 1133 1 SOPOAVPPYASENOTCRDOEOSDTTCKNPLEPLPDFMSGT 197	
	Title: Perfect score: Sequence:	

562222 seqs, 172994929 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

562222 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_rvirus:*
sp_bacteriap:*
sp_archeap:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					•													
		Description	016042 homo sapien	091zm6 rattus norv	062327 mus musculu	095407 homo sapien	088734 mus musculu	O9byu0 homo sapien	099ne0 mus musculu	O99nel mus musculu	O99ne2 mus musculu	Q9xsz8 cercopithec	008712 mus musculu	072735 cowpox viru	O9uhp4 homo sapien	000300 homo sapien	OgpusO salvelinus	008727 rattus norv
)B ID	4 016042	11 Q912M6	11 062327	4 095407	11 088734	4 Q9BYU0	11 Q99NE0	11 099NE1	11 Q99NE2	6 Q9XSZ8	11 008712	12 072735	4 Q9UHP4	4 000300	13 Q9PUS0	11 008727
		Match Length DB	425	433	459	300	482	203	260	222	234	283	401	186	372	401	302	401
æ	Query	Match	25.7	25.7	25.6	25.3	24.4	22.3	22.2	21.5	21.5	21.4	21.4	21.2	21.1	21.1	21.0	20.8
		Score	291.5	291.5	290	285.5	276.5	252.5	251.5	243.5	243.5	242.5	242.5	240	239.5	239.5	238	235.5
	Result	No.	н	7	٣	4	2	Q	7	œ	6	10	11	12	13	14	15	16

8;

15 TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLFICQLC 74

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096631 090000 07117 090000 075509 091000 091000 091000 091000 091000 091000 09100 00
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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111777733322222222222222222222222222222
230.5 230.5 229.5 228.5 228.5 226.5 225.5 225.5 225.5 225.5 227.2 227.2 221.3
11112222222222222222222222222222222222

ALIGNMENTS

							tomi;					tz R.,		tinct														:-	27; Gaps
							leos	o.				Gen		dis														425;	
			_	(e)			Craniata; Vertebrata; Euteleostomi;	Catarrhini; Hominidae; Homo.				Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,		"Two human TNF receptors have similar extracellular, but distinct													:RC64;	Length	Indels
	F		Last sequence update)	Last annotation update)			ertebrat	Hominic				.C., Lal		racellul			·.						1				1B24A97E3AD4CF9F CRC64;	DB 4;	3 73;
	425 AA.	3)	edneuce	notatio	TUMOR NECROSIS FACTOR RECEPTOR (FRAGMENT).		iata; Ve	rrhini;				, Pan Y		lar ext													4A97E3A	Score 291.5;	24; Mismatches 73
	PRT;	Created)	Last se	Last a	OR (FR		i; Cran	; Cata			6549;	ler U.		e simi	ces.";						:		1, 1.	2; 3.				Score	7. Mis
	.RY;	1. 01,	(TrEMBLrel. 17,	1. 17,	RECEPT		Eukaryota; Metazoa; Chordata;	Mammalia; Eutheria; Primates;			MEDLINE=91370690; PubMed=1966549;	H., Guk	Brockhaus M., Lesslauer W.;	ors hav	intracellular, domain sequences.";	. (06	EMBL; S63368; AAB19824.2;		InterPro; IPR001368; TNFR_c6.	6; 4.	ProDom; PD000771; INFR_c6; 1	4.	'R_NGFR	PROSITE; PS50050; TNFR_NGFR_2;	,	_	44608 MW;	25.78;	ρ T
	PRELIMINARY;	(TrEMBLrel.	EMBLre	EMBLre	FACTOR	uman).	zoa; C	ria; P		Ą.	0; Pub	scher	esslan	recept	domain	237(19	AB1982	CDF.	1368;	TNFR_C	1; TNF	TNFR;	2; TNF	O; TNF				1	servat
	PRE			101 (Tr	ROSIS	ens (H	; Meta	Euthe	9096 - 0	FROM N	137069	, Loet	Μ., Γ	IN TNF	ular,	2:231-	368; A	942; 1	IPR00	0000;	ללסססםי	100208;	PS0065	PS5005	•	_	425 AA;	1 7 7 7	65; Conservative
1	Q16042 Q16042;	01-NOV-1996	01-JUN-2001	01-JUN-2001	4OR NEC	Homo sapiens (Human)	aryota	umalia;	NCBI_TaxID=9606;	SECUENCE FROM N.A.	LINE-9	bic Z.	ckhaus	vo huma	racell	okine	3L; S63	HSSP; P25942; 1CDF.	:erPro;	Pfam; PF00020; TNFR_c6; 4.	Dom; P	ART; SM	SITE;	SITE;	Receptor.	NON_TER	SEQUENCE	Query Match	ss 65
RESULT Q16042																											-	Query	Matches (
× O	H N	ď	DŢ	D	DE	os	8	8	O Z	RP	X	RA	RA	RT	R	R	DR	DR	DR	DR	DR	DR	DR	DR	3	H	S		

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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE-99087326; PubMed-9872321;
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87
93
268
345
421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 VC----APESPTLS 195
                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
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Matches 65; Conserv
                                                                                                                                                                       Genomics 0:0-0(0).
                                                              SEQUENCE FROM N.A.
                       NCBI_TaxID=10090;
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                                                                 STRAIN-SPRAGUE-DAWLEY;
OSDURG B., Pelser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
OSDURG B., Pelser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
TWF-receptors p60 and p80 are constitutively expressed by rat brain capillary endothelial cells and participate in TWF-alpha transport through the blood-brain barrier.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF420214; AAL16021.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 LTICOLC-RPC--DPVMGLEEIAPCTSKRKTQCRCQPGMFCA--AWALECTHCELLSDCP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 LHTCLSCSSSCSDDQV----ETHNCTKKQNRVCACNADSYCALKLHSGNCRQCMKLSKCG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 EAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEÅAPGTAQSDTTC--
3 TCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSC
                                         75 R---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLSDCPPG----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.7%; Score 291.5; DB 11; Length 433; 33.3%; Pred. No. 1.8e-23;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MURINE TUMOUR NECROSIS FACTOR RECEPTOR 2 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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0-10EC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91;
                                                                                                                                                                                                                                                                                                                                                               433 AA.
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45723 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 CKNPLEPLPPEMSGT 197
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                                                                                                                                                                                                            184 KNPLEPLPP 192
                                                                                                                                                                                                                                                 167 TSPTRSMAP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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SEQUENCE
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Q62327;
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Matches
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67 YLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA--AWALECTHCELLSDC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 PYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWN
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                         2 is
                                                                                                                                                                             Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.; "Allelic variation of the type 2 tumor necrosis factor receptor
Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
"Amino acid variation in the tumor Nerosis factor receptor
linked to autoimmune diabetes in NOD mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catarrhini; Hominidae; Homo
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-> F.
-> C.
6C5lD2CFlC4626DF CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1)
FACTOR RECEPTOR SUPERFAMILY, MEMBER 6B, DECOY).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.6%; Score 290; DB 11;
33.5%; Pred. No. 2.8e-23;
live 24; Mismatches 85
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                                                                                                                                      STRAIN=NOD;
MEDLINE=95178848; PubMed=7873884;
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                                                                                                                                                                                                                                                                                                          InterPro; IPR001368; TWR_c6.
Pfam: PF00020; TWFR_c6; 4.
ProDom: PD000771; TWFR_c6; 1.
SMART; SM0208; TWFR; 4.
PROSITE: PS00652; TWFR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_2; 3.
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Mammalia; Eutheria; Primates;
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EMBL; X76401; CAA53981.1; -.
HSSP; P19438; INCF.
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482 AA.

PRT;

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Receptor.
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Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Botstein D., Sakkenazi A.; "Genomic amplification of a decoy receptor for Fas ligand in lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-2012600; PubMed-10655513; MEDLINE-20125600; PubMed-10655513; MEDLINE-20125600; MEDLINE-20125600; MEZKER M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.; "Overexpression of M68/DcR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.2%; Score 285.5; DB 4; Length 300; 36.0%; Pred. No. 5.7e-23; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 LEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCV 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 PCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKN----PLEPLPP 192
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                                                                                                                                                                                                                              MEDLINE-99253915; PubMed-10318773;
Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
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TISSUE=LUNG CARCINOMA, LARGE CELL UNDIFFERENTIATED.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
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PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF217793; AAF33685.1; -- AF217794; AAF33685.1; -- AL121845; CAC03668.1; -- BC017065; AAH17065.1; -- O14763; 1D0G.
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ProDom; PD000771; TNFR_c6; 1.
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                                                                                                                                         Nature 396:699-703(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-2000)
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Submitted (NOV-2001)
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Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                TISSUE-BLOOD
                                                                                                                        colon cancer
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SEQUENCE
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RESULT 088734

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MEDLINE-98414512; PubMed-9740674;

MEDLINE-98414512; PubMed-9740674;

MEDLINE-98414512; PubMed-9740674;

MEDLINE-98414512; PubMed-9740674;

MEDLINE-98414512; PubMed-9740674;

MEDLINE-98414512; PubMed-9740674;

MEDLINE-98414619; CAA74969; MEDLINED.

MEDLINE-984199; CAA74969; MEDLINED.

MEDLINE-984199; MARA74969; MEDLINED.

MEDLINE-984199; MARA74969; MEDLINED.

MEDLINE-984199; MARA74969; MEDLINED.

MEDLINE-98499; MARA74969; MAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
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SEQUENCE FROM N.A.
MEDLINE=21117110; PubMed=11172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482 AA; 51106 MW; F6C15046B48FF83C CRC64;
                                    Last sequence update)
Last annotation update)
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Last annotation update)
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   Created)
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                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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08,
19,
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01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
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                                    (TrEMBLrel.
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(TrEMBLrel.
                                                                    01-DEC-2001 (TrEMBLrel
P80 TNF-ALPHA RECEPTOR
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                                                                                                                                                                         Mus musculus (Mouse)
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Best Local Simi
Matches 65;
01-NOV-1998
                                    01-NOV-1998
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Best Local Similarity 31.7%
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  22 PPTA----CR--EKQYLINSQ--CCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWN 72
                                                                                                                                                                                                                                                                                                                                                            7 PPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RA TONE W. Waldmann H.;

REQUENCE FROM N.A.

REGULAIN-111710; PubMed=11172023;

RA TONE M., Tone Y. Fairchild P.J., Wwkes M., Waldmann H.;

REGULAIN-111710; PubMed=11172023;

RA TONE M., Tone Y. Fairchild P.J., Wwkes M., Waldmann H.;

RI Alternative splicing.";

R. Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

EMBL; AJ401390; CAC29430.1; -.

BR HSSP; P25941; LCDF.

DR HSPS; P25942; LCDF.

DR InterPro; IPR001005; Ribosomal_S2.

InterPro; IPR001005; Ribosomal_S2.

DR Pfam; PF00020; TNFR.C6; 1.

DR Probom; PD000771; TNFR.C6; 1.

DR PROSITE; PS00037; RTPR_C6; 1.

DR PROSITE; PS000652; RIBCSOMAL_S2_1; UNKNOWN_1.

DR PROSITE; PS000652; RIBCSOMAL_S2_1;

DR PROSITE; PS000652; TNFR_NGFR_1; 1.

PROSITE; PS000652; TNFR_NGFR_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                            31;
*Regulation of CD40 function by its isoforms generated through
                                                                                                                                                                                                                                                                                       Query Match 22.3%; Score 252.5; DB 4; Length 203; Best Local Similarity 33.2%; Pred. No. 1.5e-19; Matches 63; Conservative 21; Mismatches 75; Indels 31.
              alternative splicing.";

Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

REMEL, AJ300189; CAC29424.1;

RISSP: P25942; ICDF.

R InterPro; IPR000561; EGF-like.

R InterPro; IPR001368; TNFR_C6.

R Prodom; P000077; TNFR_C6; 1.

R PROSITE; SM00208; TNFR; 4.

R PROSITE; PS00186; TNFR, 4.

R PROSITE; PS0655; TNFR, 4.

R PROSITE; PS06505; TNFR_NGFR_1; 1.

R PROSITE; PS06505; TNFR_NGFR_1; 1.

R PROSITE; PS06050; TNFR_NGFR_2; 3.

SEQUENCE 203 AA; 22259 WW; 0739955F79D59AF CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CD40 TYPE V ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 AA
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181 LRDPVC-HPL 189
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Q99NE0;
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                                                                                                                                                                                           75 RPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPG-----TEAEL 129
                                                                                                                                                                                                                             130 KDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC----KN 185
                                                                                                                                                                                                                                                                                                                                   139 TDTV-----CHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVICEKVVKK 192
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                                                                                  15 TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC
                                                                                                                 25 TCSD--KQYLHDGQ--CCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQH
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-2117110; PubMed-11172023;
MEDLINE-2117110; PubMed-11172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
Tone M., Tone Code function by its isoforms generated through atternative splicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
ENBL: AJ401389; CAC29429.1;
HSSP: P25942; ICDF.
HIGFPRO; IPRO01005; Myb_DNa_bind.
InterPro; IPRO01065; Myb_DNa_bind.
InterPro; IPRO01065; Thread.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 KDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 222;
31.7%; Pred. No. 2.4e-19;
iive 22; Mismatches 84; Indels
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.5%; Score 243.5; DB 1.31.0%; Pred. No. 1.5e-18; iive 22; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodom: PF00020; TNFR_66; 4.

Prodom: PD000771; TNFR_66; 1.

SMART; SM00208; TNFR; 4.

PROSITE: PS00037; MYB_1; UNKNOWN_1.

PROSITE: PS00052; RIBOSOMAL_S2_1; UNKNOWN_1.

PROSITE: PS00062; TNRR_NGFR_1; 1.

SEQUENCE 222 AA; 244.99 WW; EE21E6C76FB42)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TIEMBLEEL 17, 101-JUN-2001 (TIEMBLEEL 17, 101-DEC-2001 (TIEMBLEEL 19, 150-1040 TYPE IV ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                             186 PL--EPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 PKDNEMLPP 201
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DB 11; Length 260;

Score 251.5;

22.28;

Query Match

Fri

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01-JUL-1997
01-JUL-1997
                                                                                                                                       Query Match
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                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                        148
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008712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 RPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPG-----TEAEL 129
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 15 TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 TCSD--KQYLHDGQ--CCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQH 80
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecus aethiops (Green monkey) (Grivet).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 KDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 TDTV-----CHPCPVGFFSNQSSLFEKCYPWISCEDKNLEVLOKGTSQTNVIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                        .17;
                                                                                                                                                             MEDLINE=21117110; PubMed=11172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
"Regulation of CD40 function by its isoforms generated through
                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                        81; Indels
                                                                                                                                                                                                                                                                                                                                                               00DB1DD38347E325 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                              aitérnative splicing.";
Proc. Natl. Acad. Scl. U.S.A. 98:1751-1756(2001).
EMBL; AJ401388; CAC29428.1; -.
HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                 21.5%; Score 243.5; DB 1
31.0%; Pred. No. 1.6e-18;
iive 22; Mismatches 81
            234 AA.
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                                                                                                                                                                                                                                                                                                                               UNKNOWN 1
                                   Created)
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MEDLINE=99296730; PubMed=10366573;
                                                                                                                                                                                                                                                                                                                            PROSITE; PS00962; RIBGSOMAL_S2_1;
PROSITE; PS00623; TNRR_NGFR_1; 1.
PROSITE; PS50050; TNRR_NGFR_2; 4.
SEQUENCE 234 AA; 25747 WW; 00D
                                                                                                                                                                                                                                          InterPro; IPR001005; Myb_DNA_bind.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001865; Ribosomal_S2.
Pfam; PF00020; INFR_c6.
ProDom; PF0000771; TNFR_c6; 4.
                                                                                                                                                                                                                                                                                                      SM00208; TNFR; 4.
E; PS00037; MYB_1; UNKNOWN_1
                             .....z001 (TrEMBLrel. 17, C. 01-DEC-2001 (TrEMBLrel. 19, La. CD40 TYPE III ISOFORM. CD40. Mis. ...
                                                                                                                                                                                                                                                                                                                                                                                                                        54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
            PRELIMINARY;
                                                                                          musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=KIDNEY
                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09XSZ8
            099NE2
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Q9XSZ8
Q99NE2
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STRAIN=BALB/C; TISSUE-KIDNEY;
STRAIN=BALB/C; TISSUE-KIDNEY;
MEDLINE=97262071; PubMed=9108485;
Simonet W. S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
Higashio K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 TICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAW-ALECTHCELLSDCPPGTEA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 SKCLQCQMCDPAMGLRTSRNCSTTANALCGCSPGHFCIIQDGDHCAACRAYATSSPG--- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis."; Gene 215:339-343(1998).
-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGE OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 YASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 ELKDEVGKGNNH-----CVPCKAGHFONTSSPSARCOPHTRCENGGLVEAAPGTAQS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---QRVQKGGTESQDTLCQNCPPGTF-SSNGTLEECQHĞNKCSKWLVTEAGPGTSSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TIEMBLIE). 04, Last sequence update)
01-JUN-2001 (TIEMBLIE). 17, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * STROMAL CELLS AND OSTEOCLAST PROGENITORS.
-1: SUBGUILT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
-1: SUBCELLULAR LOCATION: EXTRACELLULAR.
-1: TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                      21.4%; Score 242.5; DB 6; Length 283; 32.2%; Pred. No. 2.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                              397951C6617FE3AA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Mismatches
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MEDLINE=98382527; PubMed=9714833;
                                                                                                                                                                                                                                         PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
SEQUENCE 283 AA; 30199 MW;
                                                                                                    InterPro; IPR001368; TNFR_c6.
Pfam; PF000020; TNFR_c6; 3.
ProDom; PD00071; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
Virology 258:365-374(1999).
EMBL; AF147720; AAD37381.1;
HSSP; O14763; 1D0G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 04, (TrEMBLrel. 04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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NCBI_TaxID=9606;
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                                                                                                                                    STRAIN-GRI-90
                                                                  A53R PROTEIN.
                         072735
072735;
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Q9UHP4
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          12
         RESULT
072735
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BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND PLACEWTA. NOT DETECTED IN SPLEEN.

-!- DEVELOPMENTAL STRAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 VMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNH 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOSVKO--ECNRTHNRVCECEEGRY-----LEIEFCLKHRSCPPGS-GVVQAGTPERNTV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 YYEPQ--HRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRP-CDP 79
                                                                                                                                                                                                                                                                          BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                        SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                      D (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                     -> R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                       -> A (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                         R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.4%; Score 242.5; DB 11; Length 401; 29.6%; Pred. No. 3.4e-18; Ive 25; Mismatches 83; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA6102D3B312470 CRC64;
                                                                                                                                                                                                                    OSTEOPROTEGERIN.
                                                                                                                                                                                                                                           TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
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TNFR-CYS 1.
                                                SWISS).
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SWISS)
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InterPro; IPR001488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF0020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 AA; 45923 MW;
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63
106
143
201
201
365
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62
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                                                                                                          P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 50; Conserv
                                 15 TO DAY 17.
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DISULFID
DISULFID
DISULFID
CARBOHYD
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63 EHWNYLTICOLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA---AWALECTHCELLS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYN 62
                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 PTPLPPHAPVNGSC--DEGEYLDKRHNQCCNQCPPGEFAKVRCSGSDNTKCERCPPHTYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       He Z. Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
"Cloning and Expression of Osteoprotegerin from Homo sapiens.";
Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
EMBL; AF134187; AAF20168.1;
HSSP; PS5942; LCDF.
InterPro; IPR000488; Death.
InterPro; IPR0001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98229462; PubMed-9568042; Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A., Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A., Ryazankina O.I., Gultorov V. N., Kotwal G.J.; Species-specific differences in genome organization of cowpox, "Species-specific differences in genome organization of cowpox,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.2%; Score 240; DB 12; Length 186; 32.2%; Pred. No. 3e-18; ive 25; Mismatches 66; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D2342F1040A00AE3 CRC64;
                                                         Created)
Last sequence update)
Last annotation update)
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0STEOPROTEGERIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AA.
   186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 DCPPGTEAELKDEVGKGNNHCVPCKAGHF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 RCPCGYFGGIDEQ---GNPICKSCCVGEY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 smallpox, and vaccinia viruses.";
Virology 243:432-460(1998).
EMBL, Y15035, CAA75273.1; ...
HSSP; P25942; LOPF.
InterPro; IPR001368; TNFR_C6.
ProDom; PR000020; TWFR_C6; 2.
ProDom; P000071; TNFR_C6; 1.
SMART; SM00208; TNFR; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00652; TNPR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
SEQUENCE 186 AA; 20482 MW;
                                                      01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 32.25
Matches 48; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                  Cowpox virus (CPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        Orthopoxvirus.
NCBI_TaxID=10243;
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DISULFID
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REPEAT
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Q9PUS0
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MEDLINE-97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Lucthy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-LUNG FIBROBLAST;
MEDLINE=98151033; PubMed=9492069;
Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Hiqashio K.;
"Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
                                                                                                                                                                                                                                                                                                                                                                                                84 EEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                      KQ--ECNRTHNRVCECKEGRY----LEIEFCLKHRSCPPGF-GVVQAGTPERNTVCKRC 124
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                     EPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRP-CDPVMGL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0STEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
TUFRSF11B OR OPG OR OCIF.
                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                        Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashlo K., "Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor."; Eur. J. Biochem. 254:685-691(1998).
                                                                                                                                                                                                                                                                      84; Indels
Pfam; PF00020; TNFR_c6; 3.

ProDom; PD000771; TNFR_c6; 1.

SMART; SM00005; DEATH; 1.

PROSITE; PS00509; TNFR, 4.

PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.

PROSITE; PS00690; TNFR_NGFR_2; 2.

NON_TER 1 1 1 SEQUENCE 372 AA; 42758 WW; F02527ASCD01CCD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 KAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSE 169
                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                      21.1%; Score 239.5; DB 4
30.9%; Pred. No. 6.8e-18;
ive 21; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                   51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
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000300
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Matches
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FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERPUTING CELL-FO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENTYORS... SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 EEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYV 93
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-!-STMILMAILI).
-!-STMILMAILI).
-!-STMILMAILI).
-!-STMILMAILI).
-!-STMILMAILI).
-!-TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
KTDNEY, PLACENTA, THYROLD. SPINAL COND AND LIVER. ALSO DETECTED
A NUMBER OF OTHER HEMATOPOLIFICA AND IMMUNE ORGANS. NOT DETECTED
THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES
-!-STMILMAITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL, AB00882; BAA32076.1; --
EMBL, AB00882; BAA32076.1; --
EMBL, U94332; AAB53709.1; --
HSSP, P25942; ICDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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Pred: No. 7.3e-18;
1; Mismatches 84; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 KAGHFONTSSPSARCOPHTRCENQGLVEAAPGTAQSDTTCKNPLE 188
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N-LINKED (GLCNAC.
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30.9%; Pred: No. 7.3e-
tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00652; TITE, NGFR_1; UNKNOWN_1.
PROSITE; PS00509; TNFR_NGFR_2; 2.
Glycoprotein; Repeat; Cytokine; Signal.
SIGNAL 1 21 BY SIMILARITY.
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TNFR-CYS 3.
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InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
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SMART; SM00208; INFR; 4.
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                                                                                                                                                        SIMILARITY)
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 TSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNH----CVPCKA 145
                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=20111091; PubMed=10642582;
Bobe J., Goetz F.W.;
"A tumor necrosis factor decoy receptor homologue is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 IVCDRCPPGTYLRAPCSAMRKSDCAECPNGAYTEFWNHISKCLRCSMCAENQVVKQ--EC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 ICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPC 89
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DECOY TWE RECEPTOR.
Salvelinus fontinalis (Brook trout) (Brook char).
Salvelinus fontinalis (Brook trout), Carok char).
Actinopterygii, Metazoa, Chordett, Craniata, Vertebrata; Euteleostomi, Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
MCBL_TaxID=8038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.0%; Score 238; DB 13; Length 302; 31.6%; Pred. No. 8e-18; ... 1ve 22; Mismatches 72; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 AA; 34037 MW; E44C73477F05C3DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 GHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 GFYSEVSSAKATCLAQSNCKVGGLRVVLKGQDWHNTLC 181
                                                                                                                                                                                                                                                                                                  BUOL Reprod. 62:420-426(2000).
EMBL; AF156738; AAD56428.1; -.
HNSSP, 014763; 1D4V.
INTECPRO; IPR000561; BGF-11ke.
INTECPRO; IPR001568; TNFR_C6.
Friam, PF000203; TNFR_C6, 4.
PRODICM; PD000771; TNFR_C6; 1.
SWART; SW00208; TNFR; 4.
PROSITE; PS00186; EGF_2; UNKNOWN_1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 31.6%
Matches 50; Conservative
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